

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:01:43 ; Search time 21 Seconds
(without alignments)
925.271 Million cell updates/sec

Title: US-09-856-796B-2

Perfect score: 1047

Sequence: 1 MATGRTSLLAFGLLCLPW.....KVETFLIRVQKSRVSGSGF 202

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1024.5 | 97.9 | 217 | 1 | STHU |
| 2 | 981.5 | 93.7 | 217 | 2 | I67410 |
| 3 | 939.5 | 89.7 | 217 | 1 | STHUV |
| 4 | 873.5 | 83.4 | 217 | 2 | E32435 |
| 5 | 872.5 | 83.3 | 217 | 1 | LCUUC |
| 6 | 866.5 | 82.8 | 217 | 2 | I67409 |
| 7 | 850.5 | 81.2 | 217 | 2 | I53267 |
| 8 | 843.5 | 80.6 | 217 | 2 | I67411 |
| 9 | 842.5 | 80.5 | 215 | 2 | A26449 |
| 10 | 831.5 | 79.4 | 212 | 2 | I67408 |
| 11 | 779.5 | 74.5 | 199 | 2 | B32435 |
| 12 | 698 | 66.7 | 216 | 2 | I46145 |
| 13 | 694 | 66.3 | 216 | 1 | STFG |
| 14 | 687 | 65.6 | 216 | 2 | JC4632 |
| 15 | 682 | 65.1 | 216 | 2 | S49483 |
| 16 | 682 | 65.1 | 216 | 2 | B49159 |
| 17 | 679 | 64.9 | 216 | 1 | STWS |
| 18 | 677 | 64.7 | 217 | 1 | STBO |
| 19 | 672 | 64.2 | 216 | 2 | A37782 |
| 20 | 666 | 63.6 | 217 | 1 | STSH |
| 21 | 666 | 63.6 | 217 | 1 | STGT |
| 22 | 666 | 63.6 | 217 | 2 | S32682 |
| 23 | 661 | 63.1 | 216 | 1 | STRT |
| 24 | 614 | 58.6 | 256 | 1 | STHUV2 |
| 25 | 603 | 57.6 | 190 | 2 | JK0219 |
| 26 | 602 | 57.5 | 190 | 2 | PN0140 |
| 27 | 601 | 57.4 | 190 | 1 | A61584 |
| 28 | 598 | 57.1 | 190 | 2 | JS0429 |
| 29 | 596 | 56.9 | 190 | 1 | STHO |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 551 | 52.6 | 216 | 2 | S04929 | somatotropin precu |
| 31 | 550 | 52.5 | 216 | 2 | A60509 | somatotropin precu |
| 32 | 542 | 51.8 | 216 | 2 | JC1514 | somatotropin precu |
| 33 | 536 | 51.2 | 191 | 2 | A60625 | somatotropin - gre |
| 34 | 480 | 45.8 | 190 | 2 | S21750 | somatotropin - Rus |
| 35 | 471.5 | 45.0 | 215 | 2 | JS0037 | somatotropin precu |
| 36 | 467.5 | 44.7 | 215 | 2 | IS1188 | somatotropin - bul |
| 37 | 465 | 44.4 | 195 | 2 | IS1250 | somatotropin - bow |
| 38 | 449 | 42.9 | 190 | 2 | A56816 | somatotropin - bul |
| 39 | 421.5 | 40.3 | 163 | 2 | JN0387 | somatotropin - sei |
| 40 | 394.5 | 37.7 | 139 | 2 | S04353 | somatotropin A - A |
| 41 | 386.5 | 36.9 | 209 | 2 | JT0483 | somatotropin I pre |
| 42 | 374.5 | 35.8 | 183 | 2 | A60623 | somatotropin - blu |
| 43 | 279.5 | 26.7 | 210 | 2 | IS0763 | somatotropin - nob |
| 44 | 279.5 | 26.7 | 210 | 2 | S21915 | somatotropin - sil |
| 45 | 278.5 | 26.6 | 210 | 2 | S69262 | growth hormone I p |

RESULT 1

STHU

somatotropin 1 precursor [validated] - human

N:Alternate names: growth hormone 1; hGH-N; pituitary somatotropin

N:Contains: growth hormone 5K peptide; somatotropin 1, long form; somatotropin 1, short form

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1984 #sequence revision 10-Feb-1995 #text change 08-Dec-2000

C:Accession: A93731; A32435; A93694; A94247; A90051; A93397; A93778; A91764; A90217; A92393

R:DeNoto, F.M.; Moore, D.D.; Goodman, H.M.

Nucleic Acids Res. 9, 3719-3730, 1981

A:Title: Human growth hormone DNA sequence and mRNA structure: possible alternative splicing

A:Reference number: A93731; MUID:82014939; PMID:6269091

A:Accession: A93731

A:Molecule type: DNA

A:Residues: 1-217 <DEN>

A:Cross-references: GB:V00520

A>Note: the 20K short form somatotropin lacks residues 58-72 (32-46 in the active hormone)

R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.

Genomics 4, 479-497, 1989

A:Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.

A:Reference number: A32435; MUID:89307277; PMID:2744760

A:Accession: A32435

A:Molecule type: DNA

A:Residues: 1-217 <CHE>

A:Cross-references: GB:J03071; NID:g183148; PIDN:AAA52549.1; PID:g183149

R:Roskam, W.; Rougeon, F.

Nucleic Acids Res. 7, 305-320, 1979

A:Title: Molecular cloning and nucleotide sequence of the human growth hormone structure

A:Reference number: A93694; MUID:80034477; PMID:386281

A:Accession: A93694

A:Molecule type: mRNA

A:Residues: 1-217 <ROS>

A:Cross-references: GB:V00519

A>Note: 35-Pro was also found

R:Martial, J.A.; Halliwell, R.A.; Baxter, J.D.; Goodman, H.M.

Science 205, 602-607, 1979

A:Title: Human growth hormone: complementary DNA cloning and expression in bacteria.

A:Reference number: A94247; MUID:79203293; PMID:377496

A:Accession: A94247

A:Molecule type: mRNA

A:Residues: 1-217 <MAR>

A:Reference number: A90048; MUID:69289202; PMID:5810834

A:Accession: A90048

A:Contents: annotation

A:Title: Human pituitary growth hormone. XIX. The primary structure of the hormone.

A:Reference number: A90051; MUID:72143935; PMID:5144027

A:Accession: A90051

A:Molecule type: protein

A;Residues: 27-94;96-217 <LIC>
R;Niall, H.D.
Nature New Biol. 230, 90-91, 1971
A;Title: Revised primary structure for human growth hormone.
A;Reference number: A93397; MUID:71139765; PMID:5279046
A;Accession: A93397
A;Molecule type: protein
A;Residues: 27-51 <NIA>
R;Niall, H.D.; Hogan, M.L.; Sauer, R.; Rosenblum, I.Y.; Greenwood, F.C.
Proc. Natl. Acad. Sci. U.S.A. 68, 866-869, 1971
A;Title: Sequences of pituitary and placental lactogenic and growth hormones: evolution
A;Reference number: A93778; MUID:71153968; PMID:5279528
A;Accession: A93778
A;Molecule type: protein
A;Residues: 119-120;157-159 <N12>
R;Niall, H.D.
in Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths, K.,
A;Title: The chemistry of the human lactogenic hormones.
A;Reference number: A94427
A;Contents: annotation; somatotropin revision
R;Bewley, T.A.; Dixon, J.S.; Li, C.H.
Int. J. Pept. Protein Res. 4, 281-287, 1972
A;Title: Sequence comparison of human pituitary growth hormone, human chorionic somatoma
A;Reference number: A91764; MUID:73092028; PMID:4675454
A;Accession: A91764
A;Molecule type: protein
A;Residues: 27-217 <BEW>
R;Lewis, U.J.; Bonewald, L.F.; Lewis, L.J.
Biochem. Biophys. Res. Commun. 92, 511-516, 1980
A;Title: The 20,000-dalton variant of human growth hormone: location of the amino acid d
A;Reference number: A90217; MUID:80130196; PMID:7356479
A;Contents: somatotropin, 20K short variant
A;Accession: A90217
A;Molecule type: protein
A;Residues: 46-57;73-80 <LEW>
R;Chapman, G.E.; Rogers, K.M.; Brittain, T.; Bradshaw, R.A.; Bates, O.J.; Turner, C.; Ca
J. Biol. Chem. 256, 2395-2401, 1981
A;Title: The 20,000 molecular weight variant of human growth hormone. Preparation and so
A;Reference number: A92311; MUID:8117361; PMID:7462247
A;Contents: somatotropin, 20K short variant
A;Accession: A92311
A;Molecule type: protein
A;Residues: 27-57;73-79 <CHA>
R;Singh, R.N.P.; Seavey, B.K.; Lewis, L.J.; Lewis, U.J.
J. Protein Chem. 2, 425-436, 1983
A;Title: Human growth hormone peptide 1-43: isolation from pituitary glands.
A;Reference number: A61466
A;Accession: A61466
A;Molecule type: protein
A;Residues: 27-69 <SIN>
R;Robson, V.M.J.; Rae, I.D.; NG, F.
Biochem. Biophys. Res. Commun. 171, 423-431, 1990
A;Title: Identification of the aspartimide structure in a previously-reported peptide.
A;Reference number: S09685; MUID:90334745; PMID:2378679
A;Accession: S09685
A;Molecule type: protein
A;Residues: 27-34, 'L', 36-47 <ROB>
R;de Vos, A.M.; Uitsch, M.; Kossiakoff, A.A.
Science 255, 306-312, 1992
A;Title: Human growth hormone and extracellular domain of its receptor: crystal structu
A;Reference number: A41728; MUID:92196577; PMID:1549776
A;Contents: annotation; X-ray crystallography, 2.8 angstroms
A;Note: the structure of the complex with growth hormone receptor is described
R;Gray, G.L.; Baldrige, J.S.; McKown, K.S.; Heyneker, H.L.; Chang, C.N.
Gene 39, 247-254, 1985
A;Title: Periplasmic production of correctly processed human growth hormone in Escherich
A;Reference number: I41126; MUID:86137393; PMID:3912261
A;Accession: I84549
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-26 <RES>
A;Cross-references: GB:M14398; NID:G183158; PIDN:AAA52554.1; PID:G183159

C;Comment: The gene for this hormone is transcribed only in somatotrophic cells of the
C;Comment: About 90% of somatotropin is the 22K long form.
A;Gene: GDB:GH1
A;Cross-references: GDB:119982; OMIM:139250
A;Map position: 17q23.1-17q23.3
A;Introns: 4/1; 57/3; 97/3; 152/3
C;Superfamily: prolactin
C;Keywords: alternative splicing; hormone; pituitary
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-217/Product: somatotropin 1, long form #status experimental <SOL>
F;27-69/Product: growth hormone 5K peptide #status experimental <SKP>
F;27-57,73-217/Product: somatotropin 1, short form #status experimental <SOS>
F;79-191,208-215/Disulfide bonds: #status experimental
Query Match 97.9%; Score 1024.5; DB 1; Length 217;
Best Local Similarity 92.6%; Pred. No. 1.2e-86;
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;
Qy 1 MATGSRRTSLLLAFGLLCIPWLQEGSAFPTPLSLFDNANLRAHRLHQLAFTDYQEF--- 57
Db 1 MATGSRRTSLLLAFGLLCIPWLQEGSAFPTPLSLFDNANLRAHRLHQLAFTDYQEPAA 60
Qy 58 -----NQTSLCFSESIPTPSNRRETOCKNLELLRISLLLIQSWLEPVOFLR 105
Db 61 YIPKEQKYQYFLQNPQTSLCFSESIPTPSNRRETOCKNLELLRISLLLIQSWLEPVOFLR 120
Qy 106 SVFANSIVYGASNSVVDLLKDLLEEGTQTLMGRLDGSPTGQIFKQYKSFDFNSHND 165
Db 121 SVFANSIVYGASNSVVDLLKDLLEEGTQTLMGRLDGSPTGQIFKQYKSFDFNSHND 180
Qy 166 ALLKNYGLLYCFKRDMDKVFTRIVQCRSVEGSGCF 202
Db 181 ALLKNYGLLYCFKRDMDKVFTRIVQCRSVEGSGCF 217
RESULT 2
167410
somatotropin - rhesus macaque
N;Alternate names: growth hormone
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
C;Accession: I67410; A05094
R;Gollos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomotropin-related complementa
A;Reference number: 153267; MUID:94008724; PMID:8404617
A;Accession: I67410
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-217 <RES>
A;Cross-references: GB:L16556; NID:G293114; PIDN:AAA18942.1; PID:G293115
R;Li, C.H.; Chung, D.; Lahm, H.W.; Stein, S.
Arch. Biochem. Biophys. 245, 287-291, 1986
A;Title: The primary structure of monkey pituitary growth hormone.
A;Reference number: A05094; MUID:86129460; PMID:3080959
A;Accession: A05094
A;Molecule type: protein
A;Residues: 27-99, 'Q', 101-178, 'D', 180-217 <LIC>
A;Note: the monkey species is not identified in the reference
R;Raben, M.S.
Science 125, 883-884, 1957
A;Title: Preparation of growth hormone from pituitaries of man and monkey.
A;Reference number: A44774
A;Contents: annotation; identification of source organism
C;Superfamily: prolactin
Query Match 93.7%; Score 981.5; DB 2; Length 217;
Best Local Similarity 88.9%; Pred. No. 1e-82;
Matches 193; Conservative 3; Mismatches 6; Indels 15; Gaps 1;
Qy 1 MATGSRRTSLLLAFGLLCIPWLQEGSAFPTPLSLFDNANLRAHRLHQLAFTDYQEF--- 57

Db 1 MAAGSRTSLLLAFALLCLPWLQEGSAFPTPLSRFDNAMLRAHRLHQLAFDTYQEFEEA 60
 QY 58 -----NPQTSLCFSESIPTPSNNRETTQKSNLELLRISLLLIQSWLEPVPQFLR 105
 Db 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNNRETTQKSNLELLRISLLLIQSWLEPVPQFLR 120
 QY 106 SVFANSLVYGASDSNVYDILLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFTDTSNHNDD 165
 Db 121 SVFANSLVYGTYSYDILLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFTDTSNHNDD 180
 QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
 Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217
 RESULT 3
 STHUV
 somatotropin 2 precursor - human
 N:Alternate names: growth hormone 2; growth hormone variant; hGH-V; placental somatotropin
 C:Contains: somatotropin 2, long splice form; somatotropin 2, short splice form
 C:Species: Homo sapiens (man)
 C:Date: 17-Dec-1982 #sequence revision 10-Feb-1995 #text_change 21-Jul-2000
 C:Accession: D32435; B28072; A01511; I52104; A60711
 R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.
 Genomics 4, 479-497, 1989
 A:Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.
 A:Reference number: A32435; MUID:89307277; PMID:2744760
 A:Accession: D32435
 A:Molecule type: DNA
 A:Residues: 1-217 <CHE>
 A:Cross-references: GB:J03071; NID:g183148; PIDN:AAA52552.1; PID:g183152
 R:Cooke, N.E.; Ray, J.; Emery, J.G.; Liebhauer, S.A.
 J. Biol. Chem. 263, 9001-9006, 1988
 A:Title: Two distinct species of human growth hormone-variant mRNA in the human placenta
 A:Reference number: A92725; MUID:88243769; PMID:3379057
 A:Accession: B28072
 A:Molecule type: mRNA
 A:Residues: 1-217 <COO>
 R:Seeburg, P.H.
 DNA 1, 239-249, 1982
 A:Title: The human growth hormone gene family: nucleotide sequences show recent divergen
 A:Reference number: A01511; MUID:83182010; PMID:7169009
 A:Accession: A01511
 A:Molecule type: DNA
 A:Residues: 1-34, 'P', 36-217 <SEE>
 R:Igout, A.; Scippo, M.L.; Franckenne, F.; Hennen, G.
 Arch. Int. Physiol. Biochim. 96, 63-67, 1988
 A:Title: Cloning and nucleotide sequence of placental hGH-V cDNA.
 A:Reference number: I52104; MUID:89024984; PMID:2460050
 A:Accession: I52104
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-217 <IGO>
 A:Cross-references: GB:M38451; NID:g183179; PIDN:AAA35891.1; PID:g183180
 R:Franckenne, F.; Scippo, M.L.; Van Beeumen, J.; Igout, A.; Hennen, G.
 J. Clin. Endocrinol. Metab. 71, 15-18, 1990
 A:Title: Identification of placental human growth hormone as the growth hormone-V gene
 A:Reference number: A60711; MUID:90317018; PMID:2196278
 A:Accession: A60711
 A:Molecule type: protein
 A:Residues: 27-44; 46-57 <PRA>
 A:Experimental source: tissue placenta
 A:Note: partial glycosylation was demonstrated by lectin binding
 C:Comment: This gene is expressed by the placenta.
 C:Genetics:
 A:Gene: GDB:GH2
 A:Cross-references: GDB:119983; OMIM:139240
 A:Map position: 17q22-17q24
 A:Introns: 4/1; 57/3; 97/3; 152/3
 C:Superfamily: prolactin
 C:Keywords: alternative splicing; glycoprotein; hormone; placenta
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-217/Product: somatotropin 2, long splice form #status predicted <SOL>

F:27-57,73-217/Product: somatotropin 2, short splice form #status predicted <SOS>
 F:79-191,208-215/Dsulfide bonds: #status predicted
 F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 89.7%; Score 939.5; DB 1; Length 217;
 Best Local Similarity 86.2%; Pred. No. 7.5e-79;
 Matches 187; Conservative 4; Mismatches 11; Indels 15; Gaps 1;
 QY 1 MATGSTRSLLLAFGLLCLPWLQEGSAFPTPLSRFDNAMLRAHRLHQLAFDTYQEFEEA 57
 Db 1 MAAGSRTSLLLAFGLLCLPWLQEGSAFPTPLSRFDNAMLRAHRLHQLAFDTYQEFEEA 60
 QY 58 -----NPQTSLCFSESIPTPSNNRETTQKSNLELLRISLLLIQSWLEPVPQFLR 105
 Db 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNNRETTQKSNLELLRISLLLIQSWLEPVPQFLR 120
 QY 106 SVFANSLVYGASDSNVYDILLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFTDTSNHNDD 165
 Db 121 SVFANSLVYGASDSNVYRHLKLEEGIQTLMGRLDGSPRTGQIFNQSYSKFTDTSNHNDD 180
 QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
 Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217
 RESULT 4
 E32435
 chorionamototropin B precursor - human
 N:Alternate names: chorionic somatomotropin 2
 C:Species: Homo sapiens (man)
 C:Date: 29-Dec-1989 #sequence revision 29-Dec-1989 #text_change 16-Jul-1999
 C:Accession: E32435
 R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.
 Genomics 4, 479-497, 1989
 A:Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.
 A:Reference number: A32435; MUID:89307277; PMID:2744760
 A:Accession: E32435
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-217 <CHE>
 A:Cross-references: GB:J03071; NID:g183148; PIDN:AAA52553.1; PID:g183153
 C:Genetics:
 A:Gene: GDB:CSH2
 A:Cross-references: GDB:119813; OMIM:118820
 A:Map position: 17q22-17q24
 C:Superfamily: prolactin
 Query Match 83.4%; Score 873.5; DB 2; Length 217;
 Best Local Similarity 79.3%; Pred. No. 8.7e-73;
 Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;
 QY 1 MATGSTRSLLLAFGLLCLPWLQEGSAFPTPLSRFDNAMLRAHRLHQLAFDTYQEFEEA 57
 Db 1 MAAGSRTSLLLAFGLLCLPWLQEGSAFPTPLSRFDNAMLRAHRLHQLAFDTYQEFEEA 60
 QY 58 -----NPQTSLCFSESIPTPSNNRETTQKSNLELLRISLLLIQSWLEPVPQFLR 105
 Db 61 YIPKQKYSFLHDSQTSFCFSDSIPTPSNMETQKSNLELLRISLLLIQSWLEPVPFLR 120
 QY 106 SVFANSLVYGASDSNVYDILLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFTDTSNHNDD 165
 Db 121 SMFANLVYDTSDDYHLLKLEEGIQTLMGRLDGSPRTGQILKQTSKFTDTSNHNDD 180
 QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
 Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217
 RESULT 5
 LCHUC
 chorionamototropin A precursor [validated] - human
 N:Alternate names: chorionic somatomotropin 1; placental lactogen
 C:Species: Homo sapiens (man)

C;Date: 23-Oct-1981 #sequence revision 23-Oct-1981 #text change 08-Dec-2000
C;Accession: C32435; A94422; I52342; A93833; A93192; A90054; A94427; A61283; I55229; I59
R;Chen, E.F.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gellinas, R.E.; Seeburg, P.
Genomics 4, 479-497, 1989
A;Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.
A;Reference number: A32435; MUID:89307277; PMID:2744760
A;Accession: C32435
A;Molecule type: DNA
A;Residues: 1-217 <CHE>
A;Cross-references: GB:J03071; NID:gt183148; PIDN:AAA52551.1; PID:gt183151
R;Goodman, H.M.; DeNoto, F.; Fiddes, J.C.; Halliwell, R.A.; Page, G.S.; Smith, S.; Tisch
in Mobilization and Reassembly of Genetic Information, Scott, W.A., Werner, R., Joseph,
A;Reference number: A94422
A;Accession: A94422
A;Molecule type: mRNA
R;Tanaka, M.; Masuda, N.; Watabiki, M.; Yamakawa, M.; Shimizu, K.; Nagai, J.; Nakashima,
Biochem. Int. 16, 287-292, 1988
A;Title: cDNA cloning of human chorionic somatomammotropin-1 mRNA whose transcription wa
A;Reference number: I52342; MUID:88209096; PMID:2835050
A;Accession: I52342
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3 <TAN>
A;Cross-references: GB:M35419; NID:g506822
R;Sherwood, L.M.; Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 76, 3819-3823, 1979
A;Title: Primary structure of the NH-2-terminal extra piece of the precursor to human pl
A;Reference number: A93833; MUID:80034970; PMID:291043
A;Accession: A93833
A;Molecule type: protein
A;Residues: 1-3-26 <SHE>
R;Experimental source: Placenta
R;Shine, J.; Seeburg, P.H.; Martial, J.A.; Baxter, J.D.; Goodman, H.M.
Nature 270, 494-499, 1977
A;Title: Construction and analysis of recombinant DNA for human chorionic somatomatro
A;Reference number: A93192; MUID:78071761; PMID:593368
A;Accession: A93192
A;Molecule type: DNA
A;Residues: 50-217 <SHI>
R;Experimental source: placenta
R;Li, C.H.; Dixon, J.S.; Chung, D.
Arch. Biochem. Biophys. 155, 95-110, 1973
A;Title: Amino acid sequence of human chorionic somatomammotropin.
A;Reference number: A90054; MUID:73201971; PMID:4712450
A;Accession: A90054
A;Molecule type: protein
A;Residues: 27-217 <LIC>
R;Experimental source: placenta
R;Niall, H.D.
in Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths, K.,
A;Title: The chemistry of the human lactogenic hormones.
A;Reference number: A94427
A;Accession: A94427
A;Molecule type: protein
A;Residues: 27-217 <NIA>
R;Experimental source: placenta
R;Nic A Baird, N.; Tipton, K.F.
Biochem. Soc. Trans. 19, 20S, 1991
A;Title: Catechol-O-methyltransferase from human placenta: purification and some propert
A;Reference number: A61283; MUID:91244006; PMID:2037148
A;Accession: A61283
A;Molecule type: protein
A;Residues: 27-46 <NIC>
R;Note: chorionammotropin apparently copurified with placental catechol-O-methyltransfer
R;Sherwood, L.M.; Handwerker, S.; McLaurin, W.D.; Lanner, M.
Nature New Biol. 233, 59-61, 1971
A;Title: Amino-acid sequence of human placental lactogen.
A;Reference number: A93401; MUID:72016313; PMID:5286363
A;Contents: annotation
R;Sherwood, L.M.; Handwerker, S.; McLaurin, W.D.; Lanner, M.
Nature New Biol. 235, 64, 1972
A;Reference number: A93405

A;Contents: annotation
R;Schneider, A.B.; Kowalski, K.; Russell, J.; Sherwood, L.M.
J. Biol. Chem. 254, 3782-3787, 1979
A;Title: Identification of the interchain disulfide bonds of dimeric human placental la
A;Reference number: A92251; MUID:79173081; PMID:438159
A;Contents: annotation; dimeric disulfide bonds
R;Selby, M.J.; Barta, A.; Baxter, J.D.; Bell, G.I.; Eberhardt, N.L.
J. Biol. Chem. 259, 13131-13138, 1984
A;Title: Analysis of a major human chorionic somatomammotropin gene. Evidence for two f
A;Reference number: I55229; MUID:85030426; PMID:6208192
A;Accession: I55229
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-217 <RES>
A;Cross-references: GB:X02401; NID:gt181120; PIDN:AAA52115.1; PID:gt181121
R;Seeburg, P.H.; Shine, J.; Martial, J.A.; Ullrich, A.; Goodman, H.
Trans. Assoc. Am. Physicians 90, 109-116, 1977
A;Title: Nucleotide sequence of a human gene coding for a polypeptide hormone.
A;Reference number: I59658; MUID:78160787; PMID:611657
A;Accession: I59658
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 160-217 <RE2>
A;Cross-references: GB:M25118; NID:gt181124; PIDN:AAA35721.1; PID:gt181125
C;Genetics:
A;Gene: GDB:CSH1
A;Cross-references: GDB:119084; OMIM:150200
A;Map position: 17q22-17q24
A;Introns: 4/1; 57/3; 97/3; 152/3
C;Superfamily: prolactin
C;Keywords: hormone; placenta
F;1-26/Domain: signal sequence #status experimental <SIG>
F;27-217/Product: chorionammotropin A #status experimental <MAT>
F;79-191/Disulfide bonds: #status experimental
F;208-215/bisulfide bonds: (in monomeric form) #status experimental
F;218/Disulfide bonds: interchain (to 215 in dimeric form) #status experimental
F;215/Disulfide bonds: interchain (to 208 in dimeric form) #status experimental
Query Match 83.3%; Score 872.5; DB 1; Length 217;
Best Local Similarity 79.3%; Pred. No. 1.1e-72;
Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;
Qy 1 MATGSRRTLLAFGLLCLPWLQEGSAFPTPLSLFNASLRAHRLHQLADTYQEP--- 57
Db 1 MAPGSRRTLLAFALLCLPWLQEGAGVQTVPLSLFDHMLQAHRAHQLADTYQEPET 60
Qy 58 -----NPQTSLCFSESPTPSNREETQKSNLELRISLLLIQSWLPEVQFLR 105
Db 61 YIPKQKYSFUDHSQTSFCFSDSIPTPSNMEETQKSNLELRISLLLIQSWLPEVQFLR 120
Qy 106 SVFANSLVYGASDSNVVDLLKDLBEGITQLMGRLEDGSPRTGQIFKQTYSPFTNSHND 165
Db 121 SMFANNLYVDTSDSDYHLLKDLBEGITQLMGRLEDGSRRTGQILKQTYSKFDINSHND 180
Qy 166 ALLKNYGLLYCFKMDKVFTEFLRIVQCRSVEGSCGF 202
Db 181 ALLKNYGLLYCFKMDKVFTEFLRIVQCRSVEGSCGF 217
RESULT 6
167409
chorionic somatomammotropin-3 - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
C;Accession: 167409
R;Golos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementa
A;Reference number: I53267; MUID:94008724; PMID:8404617
A;Accession: I67409
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-217 <RES>

A;Cross-references: GB:IL16554; NID:g293112; PIDN:AAA18841.1; PID:g293113
C;Superfamily: prolactin

Query Match 82.8%; Score 866.5; DB 2; Length 217;
Best Local Similarity 77.4%; Pred. No. 3.8e-72;
Matches 168; Conservative 14; Mismatches 20; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF 60
QY 58 -----NPQTSLCFSSSIPTPSNREETQOKSNLELLRISLLLIQSWLEPVOFLR 105
DB 61 YIPKEKHSIMGNPQASFCFESSIPTPSNREETQOKSNLELLRISLLLIQSWLEPVOFLR 120
QY 106 SVFANSLVYGASDSNVYDILLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 165
DB 121 SVFANSLVYGTSDAYDILLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 202
DB 181 SLLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 217

RESULT 7
I53267
chorionic somatomotropin-1 - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
C;Accession: I53267
R;Golos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993

A;Title: Cloning of four growth hormone/chorionic somatomotropin-related complementar
A;Reference number: I53267; PMID:94008724; PMID:8404617
A;Accession: I53267
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-217 <RES>
A;Cross-references: GB:IL16552; NID:g293108; PIDN:AAA18839.1; PID:g293109
C;Superfamily: prolactin

Query Match 81.2%; Score 850.5; DB 2; Length 217;
Best Local Similarity 75.6%; Pred. No. 1.1e-70;
Matches 164; Conservative 18; Mismatches 20; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF 60
QY 58 -----NPQTSLCFSSSIPTPSNREETQOKSNLELLRISLLLIQSWLEPVOFLR 105
DB 61 YIPKEKHSIMGNPQASFCFESSIPTPSNLEETQOKSNLELLRISLLLIQSWLEPVOFLR 120
QY 106 SVFANSLVYGASDSNVYDILLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 165
DB 121 SVFANSLVYGTSDVHLLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 202
DB 181 SLLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 217

RESULT 8
I67411
somatotropin - rhesus macaque
N;Alternate names: growth hormone
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
C;Accession: I67411
R;Golos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.
Endocrinology 133, 1744-1752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomotropin-related complementar
A;Reference number: I53267; PMID:94008724; PMID:8404617

A;Accession: I67411
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-217 <RES>
A;Cross-references: GB:IL16555; NID:g293116; PIDN:AAA20180.1; PID:g293117
C;Superfamily: prolactin

Query Match 80.6%; Score 843.5; DB 2; Length 217;
Best Local Similarity 76.5%; Pred. No. 4.9e-70;
Matches 166; Conservative 14; Mismatches 22; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF 60
QY 58 -----NPQTSLCFSSSIPTPSNREETQOKSNLELLRISLLLIQSWLEPVOFLR 105
DB 61 YIPKEKHSIMGNPQASFCFESSIPTPSNREETQOKSNLELLRISLLLIQSWLEPVOFLR 120
QY 106 SVFANSLVYGASDSNVYDILLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 165
DB 121 SVFANSLVYGTSDVHLLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 202
DB 181 TLLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 217

RESULT 9
A26449
choriomamotropin precursor (allele hcs-3) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 28-Jul-1995
C;Accession: A26449
R;Hirt, H.; Kimelman, J.; Birnbaum, M.J.; Chen, E.Y.; Seeburg, P.H.; Eberhardt, N.L.; Bar
DNA 6, 59-70, 1987
A;Title: The human growth hormone gene locus: structure, evolution, and allelic variation
A;Reference number: A26449; PMID:87161235; PMID:3030680
A;Accession: A26449
A;Molecule type: DNA
A;Residues: 1-215 <HIR>
C;Superfamily: prolactin
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-215/Product: choriomamotropin, hcs-3 allele #status predicted <MAT>

Query Match 80.5%; Score 842.5; DB 2; Length 215;
Best Local Similarity 77.9%; Pred. No. 6e-70; 19; Indels 17; Gaps 3;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFGLLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFDITYQEF 60
QY 58 -----NPQTSLCFSSSIPTPSNREETQOKSNLELLRISLLLIQSWLEPVOFLR 105
DB 61 YIPKDKYSFVHDSQTSFCFSSSIPTPSNREETQOKSNLELLRISLLLIQSWLEPVOFLR 118
QY 106 SVFANSLVYGASDSNVYDILLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 165
DB 119 SVFANSLVYGTSDVHLLKLEGIQTLMGRLDGSPRTGQIFKQYKSKFTNSHND 178
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 202
DB 179 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVGSGCF 215

RESULT 10
I67408
chorionic somatomamotropin-2 - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 16-Jul-1999
C;Accession: I67408
R;Golos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.

Endocrinology 133, 1744-1752, 1993
A;Title: Cloning of four growth hormone/chorionic somatomotropin-related complementat
A;Reference number: 153267; MUID:94008724; PMID:8404617
A;Accession: I67408
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <RES>
A;Cross-references: GB:U16553; NID:G293110; PIDN:AAA18840.1; PID:G293111
C;Superfamily: prolactin

Query Match 79.4%; Score 831.5; DB 2; Length 212;
Best Local Similarity 75.5%; Pred. No. 6.1e-69;
Matches 160; Conservative 18; Mismatches 19; Indels 15; Gaps 1;

QY 6 RTSLIAFGLLCPLPWQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEF----- 57
DB 1 RTSLIAFGLLCPLPWQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEFBEAYIPKE 60
QY 58 -----NPQTSLCFSESIPTPSNREETOQKSNLELRISILLIQSWLEPQVFLRSVFAN 110
DB 61 KKHSLMENPQASTCFADSIPTPSNLEETOQKSNLELRISILLIQSWLEPQVFLRSVFAN 120
QY 111 SLVYGASDSNVYDLLKDLLEGITQTLMGRLDGSPRTGQIFKQYTSKEDTNSHNDALLKN 170
DB 121 NLLHHTSDSDVHLLKDLLEGITLMMWRLEDGIPRTGHIFKQYTSKEDAHSONDLSLLKN 180
QY 171 YGLLYCFRKMVKVETFLRVQCRSVEGSCGF 202
DB 181 YGLHLCFRKMDVMVETFLRVQCRVTEGSCGF 212

- RESULT 11
B32435
chorionamototropin-like protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 29-Dec-1989 #sequence_revision 29-Dec-1989 #text_change 16-Jul-1999
C;Accession: B32435
R;Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.
Genomics 4, 479-497, 1989
A;Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.
A;Reference number: A32435; MUID:89307277; PMID:2744760
A;Accession: B32435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <CHE>
A;Cross-references: GB:J03071; NID:G183148; PIDN:AAA52550.1; PID:G183150
C;Superfamily: prolactin

Query Match 74.5%; Score 779.5; DB 2; Length 199;
Best Local Similarity 77.7%; Pred. No. 3.3e-64;
Matches 157; Conservative 10; Mismatches 32; Indels 3; Gaps 1;

QY 1 MATGSRSLIAFGLLCPLPWQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEFNPQ 60
DB 1 MAAGSRSLIAFALLCLPWQEGAGVQVTPSLRFLKEMQLQAHRAHQLAIDTYQEFISS 60
QY 61 TSLCFSESIPTPSNREETOQKSNLELRISILLIQSWLEPQVFLRSVFANSLVYGASDSN 120
DB 61 WGM-- -DSIPTSNREETOQKSNLELRISILLIQSWLEPQVFLRSVFANSLVYDTSDD 117
QY 121 VYDLLKDLLEGITQTLMGRLDGSPRTGQIFKQYTSKEDTNSHNDALLKNYGLLYCFRKM 180
DB 118 DYHLLKDLLEGITQTLMGRLDGSHLTGTLQYTSKEDTNSHNDALLKNYGLLYCFRKM 177
QY 181 MDKVETFLRVQCRSVEGSCGF 202
DB 178 MDKVETFLRVQCRSVEGSCGF 199

RESULT 12
I46145
somatotropin precursor - dog
N;Alternate names: growth hormone

C;Species: Canis lupus familiaris (dog)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 16-Jul-1999
C;Accession: I46145; S35790
R;Ascacio-Martinez, J.A.; Barrera-Saldana, H.A.
Gene 143, 277-280, 1994
A;Title: A dog growth hormone cDNA codes for a mature protein identical to pig growth h
A;Reference number: I46145; MUID:94266166; PMID:8206387
A;Residues: I46145
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-216 <ASC>
A;Cross-references: EMBL:Z23067; NID:G312195; PIDN:CAA80601.1; PID:G312196
A;Note: submitted to the EMBL Data Library, June 1993
C;Superfamily: prolactin
C;Keywords: hormone; pituitary
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-216/Product: somatotropin #status predicted <MAT>
F;78-189,206-214/Disulfide bonds: #status predicted

Query Match 66.7%; Score 698; DB 2; Length 216;
Best Local Similarity 64.5%; Pred. No. 1.1e-56;
Matches 140; Conservative 20; Mismatches 41; Indels 16; Gaps 3;

QY 1 MATGSRSLIAFGLLCPLPWQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
DB 1 MAAGSRSLIAFALLCLPWQEGAGVQVTPSLRFLKEMQLQAHRAHQLAIDTYQEF 60
QY 58 -----NPQTSLCFSESIPTPSNREETOQKSNLELRISILLIQSWLEPQVFLRS 106
DB 61 YIEGQRYSTQNAQAFCSETIPAPTKDQBAQORSVVELLRSLILLIQSWLGPVQFLSR 120
QY 107 VFANSLVYGASDSNVYDLLKDLLEGITQTLMGRLDGSPRTGQIFKQYTSKEDTNSHND 166
DB 121 VFTNSLVFGTSD-RVYEKLKDLLEGITQALMRELEDGSPRAGQILKQYDKFDTNLRSD 179
QY 167 LKKNYGLLYCFRKMVKVETFLRVQCRS-VEGSCGF 202
DB 180 LKKNYGLLSCLPKDLKHAETFLRVKCRFVSSCAF 216

RESULT 13
STPG
somatotropin precursor - pig
N;Alternate names: growth hormone
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999
C;Accession: J00015; S09015; I46584; I46585; PC1063; A01516; A94594
R;Vize, P.D.; Wells, J.R.E.
Gene 55, 339-344, 1987
A;Title: Isolation and characterization of the porcine growth hormone gene.
A;Reference number: J00015; MUID:89030700; PMID:3666458
A;Accession: J00015
A;Molecule type: DNA
A;Residues: 1-216 <VIZ>
A;Cross-references: GB:M17704; NID:G164475; PIDN:AAA31044.1; PID:G164476
R;Kato, Y.; Shimokawa, N.; Kato, T.; Hirai, T.; Yoshinaka, K.; Kawai, H.; Hattori, M.A.
Biochim. Biophys. Acta 1048, 290-293, 1990
A;Title: Porcine growth hormone: molecular cloning of cDNA and expression in bacterial
A;Reference number: S09015; MUID:90212663; PMID:2182128
A;Accession: S09015
A;Molecule type: mRNA
A;Residues: 1-216 <KAT>
A;Cross-references: GB:X53325; NID:G288361; PIDN:CAA37411.1; PID:G288362
R;Seeburg, P.H.; Sias, S.; Adelman, J.P.; de Boer, H.A.; Hayflick, J.; Jhurani, P.; Goe
DNA 2, 37-45, 1983
A;Title: Efficient bacterial expression of bovine and porcine growth hormones.
A;Reference number: I45898; MUID:83209123; PMID:6303731
A;Accession: I46584
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 7-8, 'V', '10-21, 'Q', '23-216 <SEE>
A;Cross-references: GB:M27326; NID:G164477; PIDN:AAA31045.1; PID:G164478
R;Su, T.

Gene 69, 81-89, 1988
A:Title: A multisite-directed mutagenesis using T7 DNA polymerase: application for recomb
A:Reference number: I46585; MUID:89137997; PMID:3224824
A:Accession: I46585
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8,'V',10-21,'Q',23-42 <SUX>
A:CROSS-references: GB:M22761; NID:6164479; PIDN:AAA31046.1; PID:6164480
R:Yang, Q.; Zhu, B.L.; Zhou, S.W.; Qi, S.Z.
Chinese J. Biotechnol. 8, 318-323, 1992
A:Title: Cloning and partly sequencing of the porcine growth hormone (pGH) gene from pit
A:Reference number: PC1063
A:Accession: PC1063
A:Molecule type: mRNA
A:Residues: 97-108,'E',110-158 <YAN>
A:Experimental source: pituitary
R:Mills, J.B.; Howard, S.C.; Scapa, S.; Wilhelm, A.E.
J. Biol. Chem. 245, 3407-3415, 1970
A:Title: Cyanogen bromide cleavage and partial amino acid sequence of porcine growth hor
A:Reference number: A01516; MUID:70293161; PMID:4918150
A:Accession: A01516
A:Molecule type: protein
A:Residues: 27-30;149-194,'N',196-216 <MIL>
R:Mills, J.B.
submitted to the Atlas, May 1971
A:Reference number: A94594
A:Accession: A94594
A:Molecule type: protein
A:Residues: 140-148 <MI2>
C:Genetics:
A:Gene: gh
A:Introns: 4/1; 57/3; 96/3; 150/3
C:Superfamily: prolactin
N:Alternate names: growth factor; growth factor; hormone
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-216/Product: somatotropin #status predicted <MAT>
F:78-189/Disulfide bonds: #status predicted
F:206-214/Disulfide bonds: #status experimental

Query Match 66.3%; Score 694; DB 1; Length 216;
Best Local Similarity 64.1%; Pred. No. 2,7e-56;
Matches 139; Conservative 20; Mismatches 42; Indels 16; Gaps 3;

QY 1 MATGRTSLLAFGLLCPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFPTYQEF--- 57
Db 1 MAAGPRNSVLLAFALLCPWPQEVGTFPAMPPLSSLFANAVLRAQHLHQLAADTYKEFERA 60

QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLRS 106
Db 61 YIPEGQYSIQNAQAFCFSETIPAPTGDKEAQRSDVELLRFSLLIQSWLGPVQFLSR 120

QY 107 VFANSLVYGASDSNYVDLLKOLEEGIQTLMGRLDGSPRTGOIFKQYTSKFDNTHNDDA 166
Db 121 VFTNSLVFGTSD-RVYEKLKOLEEGIQALMRELEDSGSPRAGQILKQTYDKFDNLRSDDA 179

QY 167 LKKNYGLLYCFRKMDKVETFLRIVQCRS-VEGSCGF 202
Db 180 LKKNYGLLSGCKKDLHKAFTYLRVMKCRFFVESSCAF 216

C:Genetics:
A:Gene: gh
A:Introns: 4/1; 57/3; 96/3; 150/3
C:Superfamily: prolactin
N:Alternate names: growth hormone
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-216/Product: somatotropin #status predicted <MAT>
F:78-189/Disulfide bonds: #status predicted
F:206-214/Disulfide bonds: #status experimental

Query Match 65.1%; Score 682; DB 2; Length 216;
Best Local Similarity 63.1%; Pred. No. 3,4e-55;
Matches 137; Conservative 21; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATGRTSLLAFGLLCPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFPTYQEF--- 57
Db 1 MAAGSWTAGLLAFALLCPWPQESAFAFPAMPPLSSLFANAVLRAQHLHQLAADTYKEFERA 60

QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLRS 106
Db 61 YIPEGQYSIQNAQAFCFSETIPAPTGDKEAQRSDVELLRFSLLIQSWLGPVQFLSR 120

QY 107 VFANSLVYGASDSNYVDLLKOLEEGIQTLMGRLDGSPRTGOIFKQYTSKFDNTHNDDA 166
Db 121 AFTNLVFGTSD-RVYEKLKOLEEGIQALMRELEDSGSPRAGQILKQTYDKFDNLRSDDA 179

QY 167 LKKNYGLLYCFRKMDKVETFLRIVQCRS-VEGSCGF 202
Db 180 LKKNYGLLSGCKKDLHKAFTYLRVMKCRFFVESSCAF 216

C:Genetics:
A:Gene: gh
A:Introns: 4/1; 57/3; 96/3; 150/3
C:Superfamily: prolactin

Query Match 65.1%; Score 682; DB 2; Length 216;
Best Local Similarity 63.1%; Pred. No. 3,4e-55;
Matches 137; Conservative 21; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATGRTSLLAFGLLCPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFPTYQEF--- 57
Db 1 MAAGSWTAGLLAFALLCPWPQESAFAFPAMPPLSSLFANAVLRAQHLHQLAADTYKEFERA 60

QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLRS 106
Db 61 YIPEGQYSIQNAQAFCFSETIPAPTGDKEAQRSDVELLRFSLLIQSWLGPVQFLSR 120

QY 107 VFANSLVYGASDSNYVDLLKOLEEGIQTLMGRLDGSPRTGOIFKQYTSKFDNTHNDDA 166
Db 121 AFTNLVFGTSD-RVYEKLKOLEEGIQALMRELEDSGSPRAGQILKQTYDKFDNLRSDDA 179

QY 167 LKKNYGLLYCFRKMDKVETFLRIVQCRS-VEGSCGF 202
Db 180 LKKNYGLLSGCKKDLHKAFTYLRVMKCRFFVESSCAF 216

C:Genetics:
A:Gene: gh
A:Introns: 4/1; 57/3; 96/3; 150/3
C:Superfamily: prolactin

Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:05:28 ; Search time 51 Seconds
(without alignments)
1235.441 Million cell updates/sec

Title: US-09-856-796B-2
Perfect score: 1047
Sequence: 1 MATGSRSTSLLLAFGLLCLPW.....KVETFLRIVQCRSVEGSCGF 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCRT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCRTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|--------|-------|--------|----|-------------------|-------------------|
| 1 | 1029.5 | 98.3 | 217 | 9 | US-09-853-688-2 | Sequence 2, Appli |
| 2 | 1029.5 | 98.3 | 217 | 9 | US-09-853-688-4 | Sequence 4, Appli |
| 3 | 1029.5 | 98.3 | 217 | 10 | US-09-969-748C-4 | Sequence 4, Appli |
| 4 | 1024.5 | 97.9 | 217 | 9 | US-09-929-918-9 | Sequence 9, Appli |
| 5 | 1017.5 | 97.2 | 217 | 9 | US-09-804-409A-16 | Sequence 16, Appl |
| 6 | 1017.5 | 97.2 | 217 | 12 | US-10-411-037-48 | Sequence 48, Appl |
| 7 | 1017.5 | 97.2 | 217 | 12 | US-10-411-026-48 | Sequence 48, Appl |
| 8 | 1017.5 | 97.2 | 217 | 16 | US-10-410-962-48 | Sequence 48, Appl |
| 9 | 1017.5 | 97.2 | 217 | 16 | US-10-411-049-48 | Sequence 48, Appl |
| 10 | 1017.5 | 97.2 | 217 | 16 | US-10-410-930-48 | Sequence 48, Appl |
| 11 | 1017.5 | 97.2 | 217 | 16 | US-10-410-997-48 | Sequence 48, Appl |
| 12 | 898.5 | 85.8 | 197 | 12 | US-10-621-693-47 | Sequence 47, Appl |
| 13 | 898.5 | 85.8 | 198 | 12 | US-10-621-693-45 | Sequence 45, Appl |
| 14 | 898.5 | 85.8 | 391 | 12 | US-10-621-693-51 | Sequence 51, Appl |
| 15 | 898.5 | 85.8 | 396 | 12 | US-10-621-693-49 | Sequence 49, Appl |

| | | | | | | |
|----|-------|------|-----|----|------------------|-------------------|
| 16 | 898.5 | 85.8 | 412 | 12 | US-10-621-693-74 | Sequence 74, Appl |
| 17 | 898.5 | 85.8 | 589 | 12 | US-10-621-693-53 | Sequence 53, Appl |
| 18 | 898.5 | 85.8 | 786 | 12 | US-10-621-693-55 | Sequence 55, Appl |
| 19 | 898.5 | 85.8 | 810 | 12 | US-10-621-693-76 | Sequence 76, Appl |
| 20 | 896.5 | 85.6 | 313 | 12 | US-10-311-473-16 | Sequence 16, Appl |
| 21 | 896.5 | 85.6 | 338 | 12 | US-10-311-473-5 | Sequence 5, Appli |
| 22 | 895.5 | 85.5 | 214 | 14 | US-10-153-207-6 | Sequence 6, Appli |
| 23 | 895.5 | 85.5 | 384 | 12 | US-10-621-693-37 | Sequence 37, Appl |
| 24 | 895.5 | 85.5 | 574 | 12 | US-10-621-693-32 | Sequence 32, Appl |
| 25 | 895.5 | 85.5 | 576 | 12 | US-10-621-693-39 | Sequence 39, Appl |
| 26 | 892.5 | 85.2 | 192 | 12 | US-10-621-693-66 | Sequence 66, Appl |
| 27 | 892.5 | 85.2 | 192 | 12 | US-10-621-693-68 | Sequence 68, Appl |
| 28 | 892.5 | 85.2 | 206 | 12 | US-10-621-693-70 | Sequence 70, Appl |
| 29 | 891.5 | 85.1 | 191 | 12 | US-10-646-798-2 | Sequence 2, Appli |
| 30 | 891.5 | 85.1 | 191 | 12 | US-10-621-693-2 | Sequence 2, Appli |
| 31 | 891.5 | 85.1 | 191 | 12 | US-10-621-693-80 | Sequence 80, Appl |
| 32 | 891.5 | 85.1 | 191 | 12 | US-10-621-693-82 | Sequence 82, Appl |
| 33 | 891.5 | 85.1 | 191 | 12 | US-10-621-693-84 | Sequence 84, Appl |
| 34 | 891.5 | 85.1 | 191 | 14 | US-10-153-207-1 | Sequence 1, Appli |
| 35 | 891.5 | 85.1 | 191 | 14 | US-10-400-377-1 | Sequence 1, Appli |
| 36 | 891.5 | 85.1 | 191 | 14 | US-10-400-708-1 | Sequence 1, Appli |
| 37 | 891.5 | 85.1 | 191 | 14 | US-10-298-148-1 | Sequence 1, Appli |
| 38 | 891.5 | 85.1 | 192 | 10 | US-09-819-094-23 | Sequence 23, Appl |
| 39 | 891.5 | 85.1 | 192 | 12 | US-10-621-693-8 | Sequence 8, Appli |
| 40 | 891.5 | 85.1 | 192 | 12 | US-10-621-693-78 | Sequence 78, Appl |
| 41 | 891.5 | 85.1 | 192 | 12 | US-10-621-693-86 | Sequence 86, Appl |
| 42 | 891.5 | 85.1 | 192 | 16 | US-10-714-067-23 | Sequence 23, Appl |
| 43 | 891.5 | 85.1 | 193 | 12 | US-10-621-693-42 | Sequence 42, Appl |
| 44 | 891.5 | 85.1 | 206 | 12 | US-10-621-693-72 | Sequence 72, Appl |
| 45 | 891.5 | 85.1 | 245 | 9 | US-09-280-030-66 | Sequence 66, Appl |

ALIGNMENTS

RESULT 1
US-09-853-688-2
; Sequence 2, Application US/09853688
; Patent No. US20020081605A1
; GENERAL INFORMATION:
; APPLICANT: COOPER, DAVID N.
; APPLICANT: PROCTER, ANNIE M.
; APPLICANT: GREGORY, JOHN
; APPLICANT: MILLAR, DAVID S.
; TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN HUMANS, THE VARIATIONS AND THEIR USES
; FILE REFERENCE: WCM78
; CURRENT APPLICATION NUMBER: US/09/853,688
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-688-2

| | | | | |
|-----------------------|-----------------|--|------------|-------------|
| Query Match | 98.3% | Score 1029.5; | DB 9; | Length 217; |
| Best Local Similarity | 93.1% | Pred No. 2.5e-99; | | |
| Matches 202; | Conservative 0; | Mismatches 0; | Indels 15; | Gaps 1; |
| Qy | 1 | MATGSRSTSLLLAFGLLCLPWLEQGSAPFTIPLSRFDNANSLRAHRLHQLAFDTYQEF | --- | 57 |
| Db | 1 | MATGSRSTSLLLAFGLLCLPWLEQGSAPFTIPLSRFDNANSLRAHRLHQLAFDTYQEF | EEA | 60 |
| Qy | 58 | -----NPTSLCFSESIPTSNREETQKSNLELLRISLLLIQSWLEPQFLR | | 105 |
| Db | 61 | YIPKEQKYSFLQNPTSLCFSESIPTSNREETQKSNLELLRISLLLIQSWLEPQFLR | | 120 |
| Qy | 106 | SVFANSLVYGASDSNVVDLLKLEEGTLMGRLEDGSPRTGQIFKQYKSFEDTNSHND | | 165 |
| Db | 121 | SVFANSLVYGASDSNVVDLLKLEEGTLMGRLEDGSPRTGQIFKQYKSFEDTNSHND | | 180 |

QY 166 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 202
Db 181 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 217

RESULT 2
US-09-853-688-4
; Sequence 4, Application US/09853688
; Patent No. US20020081605A1
; GENERAL INFORMATION:
; APPLICANT: COOPER, DAVID N.
; APPLICANT: PROCTER, ANNIE M.
; APPLICANT: GREGORY, JOHN
; APPLICANT: MILLAR, DAVID S.
; TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN HUMANS, THE VARIATIONS AND THEIR USES
; FILE REFERENCE: WCM78
; CURRENT APPLICATION NUMBER: US/09/853,688
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-688-4

Query Match 98.3%; Score 1029.5; DB 9; Length 217;
Best Local Similarity 93.1%; Pred. No. 2.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRFDNASRAHRLHQLAFDTYQEF--- 57
Db 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRFDNASRAHRLHQLAFDTYQEFEEA 60
QY 58 -----NPQTSLCFSESIPTPSNRRETOQKSNLELLRISLLIQSWLEPVOFLR 105
Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNRRETOQKSNLELLRISLLIQSWLEPVOFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKDLLEGITQMLGRLEDGSPRTGQIFKQTSYKFDNNSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKDLLEGITQMLGRLEDGSPRTGQIFKQTSYKFDNNSHND 180
QY 166 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 202
Db 181 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 217

RESULT 4
US-09-929-918-9
; Sequence 9, Application US/09929918
; Patent No. US20020090678A1
; GENERAL INFORMATION:
; APPLICANT: Kordyum, Vitaliy A.
; APPLICANT: Chernykh, Svitlana I.
; APPLICANT: Slavenchenko, Iryna Yu.
; APPLICANT: Vozianov, Oleksandr
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PHAGE.006A
; CURRENT APPLICATION NUMBER: US/09/929,918
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 09/318,288
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-929-918-9

Query Match 97.9%; Score 1024.5; DB 9; Length 217;
Best Local Similarity 92.6%; Pred. No. 8.4e-99;
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRFDNASRAHRLHQLAFDTYQEF--- 57
Db 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRFDNASRAHRLHQLAFDTYQEFEEA 60
QY 58 -----NPQTSLCFSESIPTPSNRRETOQKSNLELLRISLLIQSWLEPVOFLR 105
Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNRRETOQKSNLELLRISLLIQSWLEPVOFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKDLLEGITQMLGRLEDGSPRTGQIFKQTSYKFDNNSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKDLLEGITQMLGRLEDGSPRTGQIFKQTSYKFDNNSHND 180
QY 166 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 202
Db 181 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 217

QY 166 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 202
Db 181 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 217

RESULT 3
US-09-969-748C-4
; Sequence 4, Application US/09969748C
; Publication No. US20030161809A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; APPLICANT: BASU, Amresh
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CELLULAR BARRIERS
; FILE REFERENCE: 057220-0303
; CURRENT APPLICATION NUMBER: US/09/969,748C
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02

Query Match 98.3%; Score 1029.5; DB 9; Length 217;
Best Local Similarity 93.1%; Pred. No. 2.5e-99;
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRFDNASRAHRLHQLAFDTYQEF--- 57
Db 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRFDNASRAHRLHQLAFDTYQEFEEA 60
QY 58 -----NPQTSLCFSESIPTPSNRRETOQKSNLELLRISLLIQSWLEPVOFLR 105
Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNRRETOQKSNLELLRISLLIQSWLEPVOFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKDLLEGITQMLGRLEDGSPRTGQIFKQTSYKFDNNSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKDLLEGITQMLGRLEDGSPRTGQIFKQTSYKFDNNSHND 180
QY 166 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 202
Db 181 ALLKNGLLYCFRKMDKVFELRIVQCRSVEGSCGF 217

RESULT 5
US-09-804-409A-16
; Sequence 16, Application US/09804409A
; Patent No. US20020155100A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; TITLE OF INVENTION: EXPRESSION IN GUT
; FILE REFERENCE: 029996/027 8721
; CURRENT FILING DATE: US/09/804,409A
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-409A-16

Query Match 97.2%; Score 1017.5; DB 9; Length 217;
Best Local Similarity 92.2%; Pred. No. 4.5e-98;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;
Qy 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFLDNASLRAHRLHQLAFDTYQEF--- 57
Db 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFPDNAMLRAHRLHQLAFDTYQEFEEA 60
Qy 58 -----NPQTSLCFSESIPTPSNREETOQKSNLELRLISILLIQSWLEPVQFLR 105
Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETOQKSNLELRLISILLIQSWLEPVQFLR 120
Qy 106 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHND 180
Qy 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

RESULT 6
US-10-411-037-48
; Sequence 48, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2002-06-07
; PRIOR FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-48

Query Match 97.2%; Score 1017.5; DB 12; Length 217;
Best Local Similarity 92.2%; Pred. No. 4.5e-98;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;
Qy 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFLDNASLRAHRLHQLAFDTYQEF--- 57
Db 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFPDNAMLRAHRLHQLAFDTYQEFEEA 60
Qy 58 -----NPQTSLCFSESIPTPSNREETOQKSNLELRLISILLIQSWLEPVQFLR 105
Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETOQKSNLELRLISILLIQSWLEPVQFLR 120
Qy 106 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHND 180
Qy 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

RESULT 7
US-10-411-026-48
; Sequence 48, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT FILING DATE: 2003-04-09
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2002-06-07
; PRIOR FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-08-16
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-48

Query Match 97.2%; Score 1017.5; DB 12; Length 217;
Best Local Similarity 92.2%; Pred. No. 4.5e-98;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;
Qy 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFLDNASLRAHRLHQLAFDTYQEF--- 57
Db 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFPDNAMLRAHRLHQLAFDTYQEFEEA 60
Qy 58 -----NPQTSLCFSESIPTPSNREETOQKSNLELRLISILLIQSWLEPVQFLR 105
Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETOQKSNLELRLISILLIQSWLEPVQFLR 120
Qy 106 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTGQIFKQTYSKFDTNSHND 180
Qy 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

| | | | | | | | | | | | | |
|----|-----|--------|--------------|-----------|--------|-------|-------|-------|-------|-------|------|----------|
| Db | 1 | MATGSR | TLLAFGLCLPWN | QEGSAFTPI | PLSRFD | NAMLR | RAHR | LHQ | LAFTY | QEF | EA | 60 |
| Qy | 58 | ----- | NPOTS | LCFS | ESPT | PNRRE | TQOKS | NLELR | ISILL | TQS | WLEP | QFLR 105 |
| Db | 61 | YIPKE | QKVS | FLQNT | SLCF | SESPT | PNRRE | TQOKS | NLELR | ISILL | TQS | WLEP |
| Qy | 106 | SVFAN | SLVYG | ASD | NNYD | LKDL | BEGI | QTL | MGR | LED | SGSP | RTCGI |
| Db | 121 | SVFAN | SLVYG | ASD | NNYD | LKDL | BEGI | QTL | MGR | LED | SGSP | RTCGI |
| Qy | 166 | ALLKN | YGLLY | CFR | KMD | KVET | FLR | VQCR | SV | EGSG | CF | 202 |
| Db | 181 | ALLKN | YGLLY | CFR | KMD | KVET | FLR | VQCR | SV | EGSG | CF | 217 |

RESULT 8
US-10-410-962-48
; Sequence 48, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-48

RESULT 9
 US-10-411-049-48
 ; Sequence 48, Application US/10411049
 ; Publication No. US20040082026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Deftrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bove, Caryn
 ; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
 ; TITLE OF INVENTION: ALPHA
 ; FILE REFERENCE: 040853-01-5055
 ; CURRENT APPLICATION NUMBER: US/10/411,049
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/397,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 48
 ; LENGTH: 217
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-411-049-48

```

RESULT 10
US-10-410-930-48
; Sequence 48, Application US/10410930
; Publication NO. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Necse Technologies, Inc.
; APPLICANT: DeFezes, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi

```

```

; APPLICANT:  Bowe, Carvyn
; TITLE OF INVENTION:  INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; TITLE OF INVENTION:  BETA
; FILE REFERENCE:  040853-01-5056
; CURRENT APPLICATION NUMBER:  US/10/410,930
; CURRENT FILING DATE:  2003-04-09
; PRIOR APPLICATION NUMBER:  US 60/328,523
; PRIOR FILING DATE:  2001-10-10
; PRIOR APPLICATION NUMBER:  US 60/344,692
; PRIOR FILING DATE:  2001-10-19
; PRIOR APPLICATION NUMBER:  US 60/387,292
; PRIOR FILING DATE:  2002-06-07
; PRIOR APPLICATION NUMBER:  US 60/391,777
; PRIOR FILING DATE:  2002-06-25
; PRIOR APPLICATION NUMBER:  US 60/396,594
; PRIOR FILING DATE:  2002-07-17
; PRIOR APPLICATION NUMBER:  US 60/404,249
; PRIOR FILING DATE:  2002-08-16
; PRIOR APPLICATION NUMBER:  US 60/407,527
; PRIOR FILING DATE:  2002-08-28
; NUMBER OF SEQ ID NOS:  75
; SOFTWARE:  PatentIn version 3.2
; SEQ ID NO 48
; LENGTH:  217
; TYPE:  prt
; ORGANISM:  Homo sapiens
US-10-410-930-48

```

| | | | | |
|-----------------------|-----------------|---|------------|-------------|
| Query Match | 97.2%; | Score 1017.5; | DB 16; | Length 217; |
| Best Local Similarity | 92.2%; | Pred. No. 4.5e-98; | | |
| Matches 200; | Conservative 0; | Mismatches 2; | Indels 15; | Gaps 1; |
| Qy | 1 | MATGSRISLLIAFGLLCLPWLQEGSAPETPLSPRLFDMASIRAHRLHQLAFDVTYQEF--- | 57 | |
| Db | 1 | MATGSRISLLIAFGLLCLPWLQEGSAPETPLSPRPFDMALRAHRLHQLAFDVTYQEFEEA | 60 | |
| Qy | 58 | -----NPQTSICFSESIPTPSNREETOQKNLELLRISLLLIQSWLEPVQFLR | 105 | |
| Db | 61 | YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKNLELLRISLLLIQSWLEPVQFLR | 120 | |
| Qy | 106 | SVFANSIVYGASDSNVYDLKDLKEEGQTLMGRLEDGSPRTGQIFKQTSKFDTSNHDD | 165 | |
| Db | 121 | SVFANSIVYGASDSNVYDLKDLKEEGQTLMGRLEDGSPRTGQIFKQTSKFDTSNHDD | 180 | |
| Qy | 166 | ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSGCF | 202 | |
| Db | 181 | ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSGCF | 217 | |

RESULT 11

```

US-10-410-997-48
; Sequence 48, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Deerees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Carolyn

```

```

; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
;
; TITLE OF INVENTION: FSH
;
; FILE REFERENCE: 040853-01-5059
;
; CURRENT APPLICATION NUMBER: US/10/410,997
;
; CURRENT FILING DATE: 2003-04-09
;
; PRIOR APPLICATION NUMBER: US 60/328,523
;
; PRIOR FILING DATE: 2001-10-10
;
; PRIOR APPLICATION NUMBER: US 60/344,692
;
; PRIOR FILING DATE: 2001-10-19
;
; PRIOR APPLICATION NUMBER: US 60/387,292
;
; PRIOR FILING DATE: 2002-06-07
;
; PRIOR APPLICATION NUMBER: US 60/391,777
;

```

```

; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-997-48

```

| Query Match | 97.2% | Score 1017.5 | DB 16 | Length 217 | | |
|-----------------------|----------------|-------------------|-----------|------------|--------------------------------|--------------------------------------|
| Best Local Similarity | 92.2% | Pred. No. 4.5e-98 | | | | |
| Matches 200 | Conservative 0 | Mismatches 2 | Indels 15 | Gaps 1 | | |
| Qy | 1 | MATGSRSTSLLA | AFGLLC | CPMLQEGSA | PPTPLSLRFDNASLRARHLQLAFDTTQCF | --- 57 |
| Db | 1 | MATGSRSTSLLA | AFGLLC | CPMLQEGSA | PPTPLSLRFPDNAMLRARHLQLAFDTTQCF | EEA 60 |
| Qy | 58 | ----- | NPQTS | LCSES | PTPSNREETQCKSNLELLR | LSLLIQSWLPVQFLR 105 |
| Db | 61 | YIPKEQKYS | FLQNPQ | TSLCFSES | PTPSNREETQCKSNLELLR | LSLLIQSWLPVQFLR 120 |
| Qy | 106 | SVFANS | LVYCAS | DNVYDL | KDIEEG | QTLMGRLEDGSPRTGQIFKQTSKFDNTSHNDD 165 |
| Db | 121 | SVFANS | LVYCAS | DNVYDL | KDIEEG | QTLMGRLEDGSPRTGQIFKQTSKFDNTSHNDD 180 |
| Qy | 166 | ALLKNYG | LLYCF | FRKMDK | VETFLR | IVQCRSVEGSCGF 202 |
| Db | 181 | ALLKNYG | LLYCF | FRKMDK | VETFLR | IVQCRSVEGSCGF 217 |

RESULT 12

```

US-10-621-693-47
; Sequence 47, Application US/10621693
; Publication No. US20040059393A1
; GENERAL INFORMATION:
; APPLICANT: Gentile Biopharmaceuticals, Inc.
; APPLICANT: Bussell, Stuart
; TITLE OF INVENTION: METHODS TO CONSTRUCT MUTATIONS
; TITLE OF INVENTION: DIRECT FUSIONS OR WITH
; FILE REFERENCE: GNT-003101.P.1-US
; CURRENT APPLICATION NUMBER: US/10/621,693
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/396,466
; PRIOR FILING DATE: 2002-07-16
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-621-693-47

```

| | | |
|-----------------------|-------------------|---|
| Query Match | | 85.8%; Score 998.5; DB 12; Length 197; |
| Best Local Similarity | | 90.7%; Pred.No. 1.2e-85; |
| Matches | 176; Conservative | 1; Mismatches 2; Indels 15; Gaps 1; |
| QY | 24 | GSAFFTPIPSRLFDNASLRAHRLHQIAFDTYQBF-----NPQTSLCFSES 68 : Db 4 GGSFTPTISRLFDNAMLRAHRLHQIAFDTYQBFEAYIPKEQKYSFLQPQTSLCFSES 63 QY 69 ITPSPNRREETQQNSNLELLRISLLLTSWLEPQVLFRSVFANSIVYGASDSNVYDLAKDL 128 Db 64 ITPSPNRREETQQNSNLELLRISLLLQSWELEPQVLFRSVFANSIVYGASDSNVYDLAKDL 123 QY 129 EEGIQTLMGRLEDGSPRTGOIFKOTYSKFDTNGHNDDALLKNYGLLYCFRKMDKVETEL 188 |

```
Db 124 EEGIQLMGRLEDSPTGQIFKQTSKFDTNSHNDALLKNYGLLYCFRKMDKVETFL 183
QY 189 RIVQCRSVEGSCGF 202
Db 184 RIVQCRSVEGSCGF 197
```

```
RESULT 13
US-10-621-693-45
; Sequence 45, Application US/10621693
; Publication No. US20040059093A1
; GENERAL INFORMATION:
; APPLICANT: Gentide Biopharmaceuticals, Inc.
; APPLICANT: Bussell, Stuart
; TITLE OF INVENTION: METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENC
; TITLE OF INVENTION: DIRECT FUSIONS OR WITH LINKERS
; FILE REFERENCE: GNT-00101.P.1-US
; CURRENT APPLICATION NUMBER: US/10/621,693
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/396,466
; PRIOR FILING DATE: 2002-07-16
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-621-693-45
```

```
Query Match 85.8%; Score 898.5; DB 12; Length 198;
Best Local Similarity 90.7%; Pred. No. 1.2e-85;
Matches 176; Conservative 1; Mismatches 2; Indels 15; Gaps 1;

QY 24 GSAPFTIPLSLFDNASLRAHRLHQLAFDTYQEF-----NPQTSLCFSES 68
Db 4 GGSFPTIPLSLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFTLQNPQTSLCFSES 63
QY 69 IPTPSNREETOQKSNLELLRISLLLIQSWLEPVPQFLRSVFANSVLVYGASDSNVYDLLKDL 128
Db 64 IPTPSNREETOQKSNLELLRISLLLIQSWLEPVPQFLRSVFANSVLVYGASDSNVYDLLKDL 123
QY 129 EEGIQLMGRLEDSPTGQIFKQTSKFDTNSHNDALLKNYGLLYCFRKMDKVETFL 188
Db 124 EEGIQLMGRLEDSPTGQIFKQTSKFDTNSHNDALLKNYGLLYCFRKMDKVETFL 183
QY 189 RIVQCRSVEGSCGF 202
Db 184 RIVQCRSVEGSCGF 197
```

```
RESULT 14
US-10-621-693-51
; Sequence 51, Application US/10621693
; Publication No. US20040059093A1
; GENERAL INFORMATION:
; APPLICANT: Gentide Biopharmaceuticals, Inc.
; APPLICANT: Bussell, Stuart
; TITLE OF INVENTION: METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENC
; TITLE OF INVENTION: DIRECT FUSIONS OR WITH LINKERS
; FILE REFERENCE: GNT-00101.P.1-US
; CURRENT APPLICATION NUMBER: US/10/621,693
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/396,466
; PRIOR FILING DATE: 2002-07-16
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Artificial
```

```
; FEATURE:
; OTHER INFORMATION: synthetic sequence
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..()
US-10-621-693-51

Query Match 85.8%; Score 898.5; DB 12; Length 391;
Best Local Similarity 90.7%; Pred. No. 3e-85;
Matches 176; Conservative 1; Mismatches 2; Indels 15; Gaps 1;

QY 24 GSAPFTIPLSLFDNASLRAHRLHQLAFDTYQEF-----NPQTSLCFSES 68
Db 197 GGSFPTIPLSLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFTLQNPQTSLCFSES 256
QY 69 IPTPSNREETOQKSNLELLRISLLLIQSWLEPVPQFLRSVFANSVLVYGASDSNVYDLLKDL 128
Db 257 IPTPSNREETOQKSNLELLRISLLLIQSWLEPVPQFLRSVFANSVLVYGASDSNVYDLLKDL 316
QY 129 EEGIQLMGRLEDSPTGQIFKQTSKFDTNSHNDALLKNYGLLYCFRKMDKVETFL 188
Db 317 EEGIQLMGRLEDSPTGQIFKQTSKFDTNSHNDALLKNYGLLYCFRKMDKVETFL 376
QY 189 RIVQCRSVEGSCGF 202
Db 377 RIVQCRSVEGSCGF 390

RESULT 15
US-10-621-693-49
; Sequence 49, Application US/10621693
; Publication No. US20040059093A1
; GENERAL INFORMATION:
; APPLICANT: Gentide Biopharmaceuticals, Inc.
; APPLICANT: Bussell, Stuart
; TITLE OF INVENTION: METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENC
; TITLE OF INVENTION: DIRECT FUSIONS OR WITH LINKERS
; FILE REFERENCE: GNT-00101.P.1-US
; CURRENT APPLICATION NUMBER: US/10/621,693
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: US 60/396,466
; PRIOR FILING DATE: 2002-07-16
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
; NAME/KEY: MISC FEATURE
; LOCATION: (198)..(395)
; OTHER INFORMATION: sequence is repeated N-1 times, where N is a positive whole numb
US-10-621-693-49

Query Match 85.8%; Score 898.5; DB 12; Length 396;
Best Local Similarity 90.7%; Pred. No. 3.1e-85;
Matches 176; Conservative 1; Mismatches 2; Indels 15; Gaps 1;

QY 24 GSAPFTIPLSLFDNASLRAHRLHQLAFDTYQEF-----NPQTSLCFSES 68
Db 4 GGSFPTIPLSLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFTLQNPQTSLCFSES 63
QY 69 IPTPSNREETOQKSNLELLRISLLLIQSWLEPVPQFLRSVFANSVLVYGASDSNVYDLLKDL 128
Db 64 IPTPSNREETOQKSNLELLRISLLLIQSWLEPVPQFLRSVFANSVLVYGASDSNVYDLLKDL 123
QY 129 EEGIQLMGRLEDSPTGQIFKQTSKFDTNSHNDALLKNYGLLYCFRKMDKVETFL 188
Db 124 EEGIQLMGRLEDSPTGQIFKQTSKFDTNSHNDALLKNYGLLYCFRKMDKVETFL 183
QY 189 RIVQCRSVEGSCGF 202
```

Db |||||
 184 RIVQCRSVEGCGF 197

Search completed: July 12, 2004, 13:11:23
Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:02:48 ; Search time 22 Seconds
(without alignments)
474.020 Million cell updates/sec

Title: US-09-856-796B-2

Perfect score: 1047

Sequence: 1 MATGSRRTSLLAFGLJCLPW.....KVETFLRIVQCRSVEGSCGF 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*

5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pcp.*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 1029.5 | 98.3 | 217 | 1 | US-08-469-486-51 |
| 2 | 1029.5 | 98.3 | 217 | 2 | US-08-469-658-51 |
| 3 | 1024.5 | 97.9 | 217 | 3 | US-08-589-028-10 |
| 4 | 1024.5 | 97.9 | 217 | 3 | US-08-784-582-10 |
| 5 | 1024.5 | 97.9 | 217 | 3 | US-08-785-271-10 |
| 6 | 1024.5 | 97.9 | 217 | 3 | US-08-759-628-11 |
| 7 | 1024.5 | 97.9 | 217 | 4 | US-09-284-878-1 |
| 8 | 1024.5 | 97.9 | 217 | 4 | US-09-511-024A-1 |
| 9 | 1016.5 | 97.1 | 217 | 1 | US-08-187-756C-4 |
| 10 | 1016.5 | 97.1 | 217 | 2 | US-08-710-324A-4 |
| 11 | 1016.5 | 97.1 | 217 | 4 | US-09-411-657-4 |
| 12 | 999 | 95.4 | 198 | 1 | US-08-187-756C-5 |
| 13 | 999 | 95.4 | 198 | 2 | US-08-710-324A-5 |
| 14 | 999 | 95.4 | 198 | 4 | US-09-411-657-5 |
| 15 | 926.5 | 88.5 | 360 | 3 | US-08-784-582-73 |
| 16 | 924.5 | 88.3 | 274 | 3 | US-08-784-582-71 |
| 17 | 914 | 87.3 | 176 | 3 | US-08-791-728-2 |
| 18 | 914 | 87.3 | 176 | 3 | US-08-990-774-2 |
| 19 | 909 | 86.8 | 176 | 3 | US-08-791-728-1 |
| 20 | 909 | 86.8 | 176 | 4 | US-08-990-774-1 |
| 21 | 896.5 | 85.6 | 191 | 4 | US-09-465-461-1 |
| 22 | 891.5 | 85.1 | 191 | 4 | US-09-284-878-5 |
| 23 | 891.5 | 85.1 | 191 | 4 | US-09-462-941-1 |
| 24 | 891.5 | 85.1 | 192 | 1 | US-08-093-383-1 |
| 25 | 891.5 | 85.1 | 194 | 2 | US-08-383-621-4 |
| 26 | 891.5 | 85.1 | 194 | 3 | US-08-459-906-4 |
| 27 | 891.5 | 85.1 | 241 | 4 | US-09-424-620B-25 |

28 891.5 85.1 245 4 US-09-280-030-66
29 884.5 84.5 401 4 US-09-420-819-36
30 881.5 84.2 191 4 US-09-554-451-1
31 880.5 84.1 177 1 US-08-187-756C-6
32 880.5 84.1 177 2 US-08-710-324A-6
33 880.5 84.1 177 4 US-09-411-657-6
34 878.5 83.9 400 4 US-09-420-819-37
35 876.5 83.7 191 3 US-08-800-215C-16
36 871.5 83.2 191 4 US-09-554-451-3
37 867.5 82.9 191 3 US-08-800-215C-18
38 867.5 82.9 191 3 US-08-800-215C-20
39 866.5 82.8 191 4 US-09-511-024A-4
40 860.5 82.2 191 4 US-09-511-024A-5
41 853.5 81.5 191 4 US-09-511-024A-6
42 851.5 81.3 191 4 US-09-511-024A-3
43 814.5 77.8 191 4 US-09-511-024A-9
44 778.5 74.4 191 4 US-09-511-024A-7
45 778.5 74.4 191 4 US-09-511-024A-8

ALIGNMENTS

RESULT 1
US-08-469-486-51
; Sequence 51, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holte, Thor Las
; APPLICANT: Ezerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-51

Query Match 98.3%; Score 1029.5; DB 1; Length 217;
Best Local Similarity 93.1%; Pred. No. 1.4e-108;

| | |
|---|---|
| Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1; | |
| QY | 1 MATGSR TSLLLAFGLCLPWLQEGSAFPTIPLSR LFDNASLRAHRLHQLAFDTYQEF-- 57 |
| Db | 1 MATGSR TSLLLAFGLCLPWLQEGSAFPTIPLSR LFDNASLRAHRLHQLAFDTYQEFEEA 60 |
| QY | 58 -----NPQTS LCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 105 |
| Db | 1 MATGSR TSLLLAFGLCLPWLQEGSAFPTIPLSR LFDNASLRAHRLHQLAFDTYQEFEEA 60 |
| QY | 58 -----NPQTS LCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 105 |
| Db | 61 YIPKEQKSYFLQNPTSLCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 120 |
| QY | 106 SVFANSLVYGASDSNVYDLLKDLEGIQTL MGRLEDGSPRTGQIFKQYTSKFDTNSHND 165 |
| Db | 61 YIPKEQKSYFLQNPTSLCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 120 |
| QY | 106 SVFANSLVYGASDSNVYDLLKDLEGIQTL MGRLEDGSPRTGQIFKQYTSKFDTNSHND 165 |
| Db | 121 SVFANSLVYGASDSNVYDLLKDLEGIQTL MGRLEDGSPRTGQIFKQYTSKFDTNSHND 180 |
| QY | 166 ALLKNYGLLYCFRDMKQVETFLRIVQCRSVEGSGCF 202 |
| Db | 181 ALLKNYGLLYCFRDMKQVETFLRIVQCRSVEGSGCF 217 |
| RESULT 2 | |
| US-08-469-658-51 | |
| ; Sequence 51, Application US/08469658 | |
| ; Patent No. 5917018 | |
| ; GENERAL INFORMATION: | |
| ; APPLICANT: Th eger sen, Hans Christian | |
| ; APPLICANT: Holtet, Thor Las | |
| ; APPLICANT: Etzerodt, Michael | |
| ; TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF | |
| ; TITLE OF INVENTION: PROTEINS | |
| ; NUMBER OF SEQUENCES: 58 | |
| ; CORRESPONDENCE ADDRESS: | |
| ; ADDRESSEE: Fish & Richardson P.C. | |
| ; STREET: 225 Franklin Street | |
| ; CITY: Boston | |
| ; STATE: Massachusetts | |
| ; COUNTRY: USA | |
| ; ZIP: 02110-2804 | |
| ; COMPUTER READABLE FORM: | |
| ; MEDIUM TYPE: Floppy disk | |
| ; COMPUTER: IBM PC compatible | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | |
| ; SOFTWARE: Patent In Release #1.0, Version | |
| ; SOFTWARE: #1.25 | |
| ; CURRENT APPLICATION DATA: | |
| ; APPLICATION NUMBER: US/08/469,658 | |
| ; FILING DATE: June 5, 1995 | |
| ; CLASSIFICATION: 530 | |
| ; PRIOR APPLICATION DATA: | |
| ; APPLICATION NUMBER: 08/192,060 | |
| ; FILING DATE: February 4, 1994 | |
| ; CLASSIFICATION: 530 | |
| ; ATTORNEY/AGENT INFORMATION: | |
| ; NAME: Paul T. Clark | |
| ; REGISTRATION NUMBER: 30,162 | |
| ; REFERENCE/DOCKET NUMBER: 06363/002002 | |
| ; TELECOMMUNICATION INFORMATION: | |
| ; TELEPHONE: 617 542 5070 | |
| ; TELEFAX: 617 542 8906 | |
| ; TELEX: 200154 | |
| ; INFORMATION FOR SEQ ID NO: 51: | |
| ; SEQUENCE CHARACTERISTICS: | |
| ; LENGTH: 217 amino acids | |
| ; TYPE: amino acid | |
| ; STRANDEDNESS: | |
| ; TOPOLOGY: linear | |
| ; MOLECULE TYPE: protein | |
| US-08-469-658-51 | |
| Query Match 98.3%; Score 1029.5; DB 2; Length 217; | |
| Best Local Similarity 93.1%; Pred. No. 1.4e-108; | |
| Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1; | |
| QY | 1 MATGSR TSLLLAFGLCLPWLQEGSAFPTIPLSR LFDNASLRAHRLHQLAFDTYQEF-- 57 |

| | |
|---|---|
| Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1; | |
| Db | 1 MATGSR TSLLLAFGLCLPWLQEGSAFPTIPLSR LFDNASLRAHRLHQLAFDTYQEFEEA 60 |
| QY | 58 -----NPQTS LCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 105 |
| Db | 61 YIPKEQKSYFLQNPTSLCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 120 |
| QY | 106 SVFANSLVYGASDSNVYDLLKDLEGIQTL MGRLEDGSPRTGQIFKQYTSKFDTNSHND 165 |
| Db | 61 YIPKEQKSYFLQNPTSLCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 120 |
| QY | 106 SVFANSLVYGASDSNVYDLLKDLEGIQTL MGRLEDGSPRTGQIFKQYTSKFDTNSHND 165 |
| Db | 121 SVFANSLVYGASDSNVYDLLKDLEGIQTL MGRLEDGSPRTGQIFKQYTSKFDTNSHND 180 |
| QY | 166 ALLKNYGLLYCFRDMKQVETFLRIVQCRSVEGSGCF 202 |
| Db | 181 ALLKNYGLLYCFRDMKQVETFLRIVQCRSVEGSGCF 217 |
| RESULT 3 | |
| US-08-589-028-10 | |
| ; Sequence 10, Application US/08589028 | |
| ; Patent No. 6087129 | |
| ; GENERAL INFORMATION: | |
| ; APPLICANT: Newgard, Christopher B. | |
| ; APPLICANT: Halban, Philippe | |
| ; APPLICANT: No. 6087129mington, Karl D. | |
| ; APPLICANT: Clark, Samuel A. | |
| ; APPLICANT: Thigpen, Anice E. | |
| ; APPLICANT: Quade, Christian | |
| ; APPLICANT: Kruse, Fred | |
| ; TITLE OF INVENTION: Recombinant Expression of Proteins From | |
| ; TITLE OF INVENTION: Secretary Cell Lines | |
| ; NUMBER OF SEQUENCES: 50 | |
| ; CORRESPONDENCE ADDRESS: | |
| ; ADDRESSEE: Arnold, White & Durkee | |
| ; STREET: P. O. Box 4433 | |
| ; CITY: Houston | |
| ; STATE: TX | |
| ; COUNTRY: USA | |
| ; ZIP: 77210-4433 | |
| ; COMPUTER READABLE FORM: | |
| ; MEDIUM TYPE: Floppy disk | |
| ; COMPUTER: IBM PC compatible | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | |
| ; SOFTWARE: Patent In Release #1.0, Version #1.30 | |
| ; SOFTWARE: #1.25 | |
| ; CURRENT APPLICATION DATA: | |
| ; APPLICATION NUMBER: US/08/589,028 | |
| ; FILING DATE: Concurrently Herewith | |
| ; CLASSIFICATION: 435 | |
| ; ATTORNEY/AGENT INFORMATION: | |
| ; NAME: Highlander, Steven L. | |
| ; REGISTRATION NUMBER: 47,642 | |
| ; REFERENCE/DOCKET NUMBER: UTSD:426\HYL | |
| ; TELECOMMUNICATION INFORMATION: | |
| ; TELEPHONE: (512) 418-3000 | |
| ; TELEFAX: (512) 474-7577 | |
| ; INFORMATION FOR SEQ ID NO: 10: | |
| ; SEQUENCE CHARACTERISTICS: | |
| ; LENGTH: 217 amino acids | |
| ; TYPE: amino acid | |
| ; STRANDEDNESS: | |
| ; TOPOLOGY: linear | |
| US-08-589-028-10 | |
| Query Match 97.9%; Score 1024.5; DB 3; Length 217; | |
| Best Local Similarity 92.6%; Pred. No. 5.1e-108; | |
| Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1; | |
| QY | 1 MATGSR TSLLLAFGLCLPWLQEGSAFPTIPLSR LFDNASLRAHRLHQLAFDTYQEF-- 57 |
| Db | 1 MATGSR TSLLLAFGLCLPWLQEGSAFPTIPLSR LFDNASLRAHRLHQLAFDTYQEFEEA 60 |
| QY | 58 -----NPQTS LCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 105 |
| Db | 61 YIPKEQKSYFLQNPTSLCFSES IPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 120 |

Best Local Similarity 92.2%; Pred. No. 4.1e-107;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;
QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
Db 1 MAAGSRSTLLAFGLLCLSWLQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEFEEA 60
QY 58 -----NPQTSICFSESPTPSNREETOQKSNLELRISLLIQSWLEPVPQFLR 105
Db 61 YIPKEQKYSFLQNPQTSICFSESPTPSNREETOQKSNLELRISLLIQSWLEPVPQFLR 120
QY 106 SVFANSLVYGASDSNVYDLKDLKEEGIQTLMGRLDGSPRTGQIFKQTSKFDNSHND 165
Db 121 SVFANSLVYGASDSNVYDLKDLKEEGIQTLMGRLDGSPRTGQIFKQTSKFDNSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

RESULT 11
US-09-411-657-4
; Sequence 4, Application US/09411657
; Patent No. 6566328
; GENERAL INFORMATION:
; APPLICANT: ROSEN, ET AL.
; TITLE OF INVENTION: Human Growth Factor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411.657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/710,324
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF104D1.SKB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-411-657-4

Query Match 97.1%; Score 1016.5; DB 4; Length 217;
Best Local Similarity 92.2%; Pred. No. 4.1e-107;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;
QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
Db 1 MAAGSRSTLLAFGLLCLSWLQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEFEEA 60
QY 58 -----NPQTSICFSESPTPSNREETOQKSNLELRISLLIQSWLEPVPQFLR 105

Db 61 YIPKEQKYSFLQNPQTSICFSESPTPSNREETOQKSNLELRISLLIQSWLEPVPQFLR 120
QY 106 SVFANSLVYGASDSNVYDLKDLKEEGIQTLMGRLDGSPRTGQIFKQTSKFDNSHND 165
Db 121 SVFANSLVYGASDSNVYDLKDLKEEGIQTLMGRLDGSPRTGQIFKQTSKFDNSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217
RESULT 12
US-08-187-756C-5
; Sequence 5, Application US/08187756C
; Patent No. 5597709
; GENERAL INFORMATION:
; APPLICANT: ROSEN, ET AL.
; TITLE OF INVENTION: Human Growth Hormone
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,756C
; FILING DATE: January 27, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-187-756C-5

Query Match 95.4%; Score 999; DB 1; Length 198;
Best Local Similarity 97.0%; Pred. No. 3.5e-105;
Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEFNPQ 60
Db 1 MAAGSRSTLLAFGLLCLSWLQEGSAFTTIPLSRLFDNASLRAHRLHQLAFDTYQEF--- 57
QY 61 TSLCFSESPTPSNREETOQKSNLELRISLLIQSWLEPVPQFLRSVFANSLVYGASDSN 120
Db 58 -SLCFSESPTPSNREETOQKSNLELRISLLIQSWLEPVPQFLRSVFANSLVYGASDSN 116
QY 121 VYDLLKDLKEEGIQTLMGRLDGSPRTGQIFKQTSKFDNSHNDALLKNYGLLYCFRKD 180
Db 117 VYDLLKDLKEEGIQTLMGRLDGSPRTGQIFKQTSKFDNSHNDALLKNYGLLYCFRKD 176
QY 181 MDKVETFLRIVQCRSVEGSCGF 202

Db 177 MDKVETFLRIVQCRSVESGCGF 198

RESULT 13

US-08-710-324A-5
; Sequence 5, Application US/08710324A
; Patent No. 5962411
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Growth Factor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,324A
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/187,756
; FILING DATE: 27-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF104D1.SKB
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-710-324A-5

Query Match 95.4%; Score 999; DB 2; Length 198;
Best Local Similarity 97.0%; Pred. No. 3.5e-105;
Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

| | | | | | |
|----|-----|--------|--|----------------------------|-----|
| QY | 1 | MATGSR | TSLLAFGLLCLPWLOEGSAFPTIPLSR | LDNLSRAHRLHQLAFDTYQEFNPQ | 60 |
| Db | 1 | MAAGSR | TSLLAFGLLCLPWLOEGSAFPTIPLSR | LDNLSRAHRLHQLAFDTYQEFNPQ | 57 |
| QY | 61 | TSLCFS | ESITPSNREETQOKSNLELLRISLLIOSWLEPVOFLRSVFANSLVYGASDSN | 120 | |
| Db | 58 | SLCFS | ESITPSNREETQOKSNLELLRISLLIOSWLEPVOFLRSVFANSLVYGASDSN | 116 | |
| QY | 121 | VYDLLK | DLKEEGITLMGRLEDGSPRTGQIFKQ | TSKFDTNSHNDALLKNYGLLYCFRKD | 180 |
| Db | 117 | VYDLLK | DLKEEGITLMGRLEDGSPRTGQIFKQ | TSKFDTNSHNDALLKNYGLLYCFRKD | 176 |
| QY | 181 | MDKVET | FLRIVQCRSVESGCGF | 202 | |
| Db | 177 | MDKVET | FLRIVQCRSVESGCGF | 198 | |

RESULT 14

US-09-411-657-5
; Sequence 5, Application US/09411657
; Patent No. 6566328
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.

; TITLE OF INVENTION: Human Growth Factor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,657
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/710,324
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF104D1.SKB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-411-657-5

Query Match 95.4%; Score 999; DB 4; Length 198;
Best Local Similarity 97.0%; Pred. No. 3.5e-105;
Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

| | | | | | |
|----|-----|--------|--|----------------------------|-----|
| QY | 1 | MATGSR | TSLLAFGLLCLPWLOEGSAFPTIPLSR | LDNLSRAHRLHQLAFDTYQEFNPQ | 60 |
| Db | 1 | MAAGSR | TSLLAFGLLCLPWLOEGSAFPTIPLSR | LDNLSRAHRLHQLAFDTYQEFNPQ | 57 |
| QY | 61 | TSLCFS | ESITPSNREETQOKSNLELLRISLLIOSWLEPVOFLRSVFANSLVYGASDSN | 120 | |
| Db | 58 | SLCFS | ESITPSNREETQOKSNLELLRISLLIOSWLEPVOFLRSVFANSLVYGASDSN | 116 | |
| QY | 121 | VYDLLK | DLKEEGITLMGRLEDGSPRTGQIFKQ | TSKFDTNSHNDALLKNYGLLYCFRKD | 180 |
| Db | 117 | VYDLLK | DLKEEGITLMGRLEDGSPRTGQIFKQ | TSKFDTNSHNDALLKNYGLLYCFRKD | 176 |
| QY | 181 | MDKVET | FLRIVQCRSVESGCGF | 202 | |
| Db | 177 | MDKVET | FLRIVQCRSVESGCGF | 198 | |

RESULT 15

US-08-784-582-73
; Sequence 73, Application US/08784582
; Patent No. 6110707
; GENERAL INFORMATION:
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Halban, Philippe A.
; APPLICANT: No. 6110707mington, Karl D.
; APPLICANT: Clark, Samuel A.
; APPLICANT: Thigpen, Anice E.
; APPLICANT: Quade, Christian
; APPLICANT: Kruse, Fred
; APPLICANT: McGarry, Dennis
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM
; APPLICANT: SECRETORY CELL LINES

```

;
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,592
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,427
; FILING DATE: 15-OCT-1996
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/589,028
; FILING DATE: 19-JAN-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
;
; REFERENCE/DOCKET NUMBER: UTSD:514
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
;
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-784-582-73

```

```

Query Match      88.5%; Score 926.5; DB 3; Length 360;
Best Local Similarity 87.6%; Pred. No. 1.5e-96;
Matches 184; Conservative 4; Mismatches 7; Indels 15; Gaps 1;

Qy      1 MATGSRISLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRHRLHQLAFDTYQEF--- 57
Db      1 MATGSRISLLAFGLLCLPWLQEGSAFPTIPLSRLFDNAMLRHRLHQLAFDTYQEFEEA 60

Qy      58 -----NFQTSLCFSESIPTPSNREETQCKSNLELLRISLLLIQSWLEPVQFLR 105
Db      61 YIPKEQKYSFTLQNPOTSLCFSESIPTPSNREETQCKSNLELLRISLLLIQSWLEPVQFLR 120

Qy      106 SVFANSLYVGASDSNVYDLLKDLREGIQTLMGLEDSGPRGTGQIFKQYKEDTNSHND 165
Db      121 SVFANSLYVGASDSNVYDLLKDLREGIQTLMGRLEDSGPRGTGQIFKQYKEDTNSHND 180

Qy      166 ALLKNYGLLYCFKDKMDKVFTRIVQCKS 195
Db      181 ALLKNYGLLYCFKDKMDKQKRSQDTTEKS 210

```

Search completed: July 12, 2004, 13:06:30
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 12:57:42 ; Search time 17 Seconds
(without alignments)
618.716 Million cell updates/sec

Title: US-09-856-796B-2
Perfect score: 1047
Sequence: 1 MATGSRSTSLLAFLGLCLPW.....KVETFLRIVQCRSVEGSCGF 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1024.5 | 97.9 | 217 | 1 | SOMA_HUMAN |
| 2 | 1018.5 | 97.3 | 217 | 1 | SOMA_PANTR |
| 3 | 981.5 | 93.7 | 217 | 1 | SOMA_MACMU |
| 4 | 955.5 | 91.3 | 217 | 1 | SOMA2_PANTR |
| 5 | 939.5 | 89.7 | 217 | 1 | SOMA2_HUMAN |
| 6 | 904.5 | 86.4 | 217 | 1 | SOMA_SAIBB |
| 7 | 895.5 | 85.5 | 217 | 1 | SOMA_CALJA |
| 8 | 872.5 | 83.3 | 217 | 1 | PL1_HUMAN |
| 9 | 829.5 | 79.2 | 217 | 1 | SOMA2_MACMU |
| 10 | 694 | 66.3 | 216 | 1 | SOMA_PIG |
| 11 | 693 | 66.2 | 216 | 1 | SOMA_HORSE |
| 12 | 687 | 65.6 | 216 | 1 | SOMA_CANFA |
| 13 | 687 | 65.6 | 216 | 1 | SOMA_FELCA |
| 14 | 682 | 65.1 | 216 | 1 | SOMA_MESAU |
| 15 | 682 | 65.1 | 216 | 1 | SOMA_RABIT |
| 16 | 679 | 64.9 | 216 | 1 | SOMA_MOUSE |
| 17 | 679 | 64.9 | 217 | 1 | SOMA_CEREL |
| 18 | 677 | 64.7 | 217 | 1 | SOMA_BOVIN |
| 19 | 672 | 64.2 | 216 | 1 | SOMA_MUSVI |
| 20 | 670 | 64.0 | 217 | 1 | SOMA_BUBBU |
| 21 | 667.5 | 63.8 | 217 | 1 | SOMA_NUCPY |
| 22 | 666 | 63.6 | 217 | 1 | SOMA_SHEEP |
| 23 | 663.5 | 63.2 | 217 | 1 | SOMA_GALSE |
| 24 | 661 | 63.1 | 216 | 1 | SOMA_RAT |
| 25 | 603 | 57.6 | 190 | 1 | SOMA_LOXAF |
| 26 | 602 | 57.5 | 190 | 1 | SOMA_BALBO |
| 27 | 601 | 57.4 | 190 | 1 | SOMA_LAMPA |
| 28 | 599.5 | 57.3 | 215 | 1 | SOMA_MONDO |
| 29 | 598.5 | 57.3 | 215 | 1 | SOMA_TRIVU |
| 30 | 598 | 57.1 | 216 | 1 | SOMA_YULVU |
| 31 | 551 | 52.6 | 216 | 1 | SOMA_ANAPL |
| 32 | 550 | 52.5 | 216 | 1 | SOMA_CHICK |
| 33 | 542 | 51.8 | 216 | 1 | SOMA_MELGA |

| | | | | | |
|----|-------|------|-----|---|-------------|
| 34 | 539.5 | 51.5 | 217 | 1 | SOMA_STRCA |
| 35 | 536 | 51.2 | 191 | 1 | SOMA_CHEMY |
| 36 | 534 | 51.0 | 190 | 1 | SOMA_CRONO |
| 37 | 496 | 47.4 | 214 | 1 | SOMA_XENLA |
| 38 | 492.5 | 47.0 | 211 | 1 | SOMA_LEPOS |
| 39 | 480 | 45.8 | 190 | 1 | SOMA1_ACIGU |
| 40 | 467.5 | 44.7 | 215 | 1 | SOMA_RANCA |
| 41 | 465 | 44.4 | 190 | 1 | SOMA2_ACIGU |
| 42 | 441.5 | 42.2 | 213 | 1 | SOMA_BUFMA |
| 43 | 432 | 41.3 | 208 | 1 | SOMB_XENLA |
| 44 | 413 | 39.4 | 206 | 1 | SOMA_PROAN |
| 45 | 389.5 | 37.2 | 209 | 1 | SOMA_ANGJA |

| | |
|--------|-------------|
| O9pwg3 | struthio ca |
| P34005 | chelonio my |
| P55755 | crocodylus |
| P12855 | xenopus lae |
| P79885 | lepisosteus |
| P26773 | acipenser g |
| P10813 | rana catesb |
| P26774 | acipenser g |
| O73849 | bufo marinu |
| P12856 | xenopus lae |
| O73848 | prototenus |
| P08899 | anguilla ja |

ALIGNMENTS

| | |
|------------|---|
| RESULT 1 | |
| SOMA_HUMAN | |
| ID | SOMA_HUMAN STANDARD; PRT; 217 AA. |
| AC | P01241; Q14405; Q16631; Q9HBZ1; Q9UMJ7; Q9UNL5; |
| DT | 21-JUL-1986 (Rel. 01, Created) |
| DT | 01-MAR-1992 (Rel. 21, Last sequence update) |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update) |
| DE | Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1). |
| DE | GH1. |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| OX | NCBI_TaxID=9606; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). |
| RX | MEDLINE=80034477; PubMed=386281; |
| RA | Roskam W., Rougeon F.; |
| RT | "Molecular cloning and nucleotide sequence of the human growth hormone structural gene."; |
| RT | Nucleic Acids Res. 7:305-320(1979). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). |
| RX | MEDLINE=79203293; PubMed=377496; |
| RA | Martial J.A., Hallewell R.A., Baxter J.D., Goodman H.M.; |
| RT | "Human growth hormone: complementary DNA cloning and expression in bacteria."; |
| RL | Science 205:602-607(1979). |
| RN | [3] |
| RP | SEQUENCE FROM N.A. (ISOFORM 1), AND POSSIBLE ALTERNATIVE SPLICING. |
| RX | MEDLINE=82014939; PubMed=6269091; |
| RA | Denoto F.M., Moore D.D., Goodman H.M.; |
| RT | "Human growth hormone DNA sequence and mRNA structure: possible alternative splicing."; |
| RL | Nucleic Acids Res. 9:3719-3730(1981). |
| RN | [4] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=83182010; PubMed=7169009; |
| RA | Seeburg P.H.; |
| RT | "The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone."; |
| RL | DNA 1:239-249(1982). |
| RN | [5] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=89307277; PubMed=2744760; |
| RA | Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., |
| RA | Gelinas R.E., Seeburg P.H.; |
| RT | "The human growth hormone locus: nucleotide sequence, biology, and evolution."; |
| RL | Genomics 4:479-497(1989). |
| RN | [6] |
| RP | SEQUENCE FROM N.A. (ISOFORM 3). |
| RC | TISSUE=Pituitary; |
| RA | Gu J., Huang Q.-H., Li N., Xu S.-H., Han Z.-G., Fu G., Chen Z.; |
| RT | "A novel gene expressed in human pituitary."; |
| RL | Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases. |

[7] SEQUENCE FROM N.A. (ISOFORM 4).
RN TISSUE=Pituitary;
RC MEDLINE=20402571; PubMed=10931946;
RX Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
axis and full-length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548 (2000).
RN [18]
RN SEQUENCE OF 1-26 FROM N.A.
RP MEDLINE=86137393; PubMed=3912261;
RX Gray G.L., Balridge J.S., McKeown K.S., Heyneker H.L., Chang C.N.;
RA Li C.H., Dixon J.S., Liu W.-K.;
RT "Human pituitary growth hormone. XIX. The primary structure of the
hormone.";
RL Arch. Biochem. Biophys. 133:70-91 (1969).
RN [10]
RN SEQUENCE OF 27-217, AND REVISIONS.
RP MEDLINE=72143935; PubMed=5144027;
RX Li C.H., Dixon J.S.;
RA "Human pituitary growth hormone. 32. The primary structure of the
hormone: revision.";
RL Arch. Biochem. Biophys. 146:233-236 (1971).
RN [11]
RN MEDLINE=73092028; PubMed=4675454;
RX Bewley T.A., Dixon J.S., Li C.H.;
RA "Sequence comparison of human pituitary growth hormone, human
chorionic somatomammotropin, and ovine pituitary growth and
lactogenic hormones.";
RL Int. J. Pept. Protein Res. 4:281-287 (1972).
RN [12]
RN SEQUENCE OF 27-61 AND 102-124.
RX MEDLINE=71139765; PubMed=5279046;
RA Niall H.D.;
RT "Revised primary structure for human growth hormone.";
RL Nature New Biol. 230:90-91 (1971).
RN [13]
RN REVISIONS TO 119-120 AND 157-159.
RX MEDLINE=71153968; PubMed=5279528;
RA Niall H.D., Hogan M.L., Sauer R., Rosenblum I.Y., Greenwood F.C.;
RT "Sequences of pituitary and placental lactogenic and growth hormones:
evolution from a primordial peptide by gene reduplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:866-869 (1971).
RN [14]
RN REVISION.
RA Niall H.D.;
RT "The chemistry of the human lactogenic hormones.";
RL (In) Griffiths K. (eds.);
RL Prolactin and carcinogenesis, Proc. fourth tenovus workshop prolactin,
pp.13-20, Alpha Omega Alpha Press, Cardiff (1972).
RN [15]
RN SEQUENCE OF 27-79 (ISOFORM 2).
RX MEDLINE=81117361; PubMed=7462347;
RA Chapman G.E., Rogers K.M., Brittain T., Bradshaw R.A., Bates O.J.,
RA Turner C., Cary P.D., Crane-Robinson C.;
RT "The 20,000 molecular weight variant of human growth hormone.
Preparation and some physical and chemical properties.";
RL J. Biol. Chem. 256:2395-2401 (1981).
RN [16]
RN SEQUENCE OF 46-80 (ISOFORM 2).
RX MEDLINE=80130196; PubMed=7356479;

RA Lewis U.J., Bonewald L.F., Lewis L.J.;
RT "The 20,000-dalton variant of human growth hormone: location of the
amino acid deletions.";
RL Biochem. Biophys. Res. Commun. 92:511-516 (1980).
RN [17]
RN DEAMINATION OF GLN-163 AND ASN-178.
RP MEDLINE=82052997; PubMed=7028740;
RX Lewis U.J., Singh R.N., Bonewald L.F., Seavey B.K.;
RA "Altered proteolytic cleavage of human growth hormone as a result of
deamidation.";
RL J. Biol. Chem. 256:11645-11650 (1981).
RN [18]
RN REVIEW.
RP MEDLINE=99321812; PubMed=10393484;
RX Baumann G.;
RA "Growth hormone heterogeneity in human pituitary and plasma.";
RL Horm. Res. 51 Suppl. 1:2-6 (1999).
RN [19]
RN 3D-STRUCTURE MODELING.
RP MEDLINE=88190073; PubMed=3447173;
RX Cohen F.E., Kuntz I.D.;
RA "Prediction of the three-dimensional structure of human growth
hormone.";
RL Proteins 2:162-166 (1987).
RN [20]
RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RP MEDLINE=92196577; PubMed=1549776;
RX de Vos A.M., Ultsch M., Kossiakoff A.A.;
RA "Human growth hormone and extracellular domain of its receptor:
crystal structure of the complex.";
RL Science 255:306-312 (1992).
RN [21]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP MEDLINE=95075462; PubMed=7984244;
RX Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
RA "The X-ray structure of a growth hormone-prolactin receptor complex.";
RL Nature 372:478-481 (1994).
RN [22]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP Chantalat L., Chirgatz N.Y., Jones N., Korber F., Navaza J.,
RA Pavlovsk A.G., Wlodawer A.;
RA "The crystal-structure of wild-type growth-hormone at 2.5-A
resolution.";
RL Protein Pept. Lett. 2:333-340 (1995).
RN [23]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=97113023; PubMed=8943276;
RA Sundstroem M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,
RA Norstedt G.;
RT "Crystal structure of an antagonist mutant of human growth hormone,
GI20R, in complex with its receptor at 2.9-A resolution.";
RL J. Biol. Chem. 271:32197-32203 (1996).
RN [24]
RN VARIANT KOWARSKI SYNDROME CYS-103.
RP MEDLINE=96150232; PubMed=8552145;
RX Takahashi Y., Kaji H., Okimura Y., Goji K., Abe H., Chihara K.;
RA "Short stature caused by a mutant growth hormone.";
RL New Engl. J. Med. 334:432-436 (1996).
RN [25]
RN ERRATUM.
RP Takahashi Y., Kaji H., Okimura Y., Goji K., Abe H., Chihara K.;
RA New Engl. J. Med. 334:1207-1207 (1996).
RN [26]
RN VARIANT KOWARSKI SYNDROME GLY-138.
RP MEDLINE=97426478; PubMed=9276733;
RX Takahashi Y., Shirono H., Arisaka O., Takahashi K., Yagi T., Koga J.,
RA Kaji H., Okimura Y., Abe H., Tanaka T., Chihara K.;
RA "Biologically inactive growth hormone caused by an amino acid
substitution.";
RL J. Clin. Invest. 100:1159-1165 (1997).
RN [27]
RN VARIANT CYS-105.
RP MEDLINE=99318093; PubMed=10391209;
RX

```

Query Match          97.9%; Score 1024.5; DB 1; Length 217;
Best Local Similarity 92.6%; Pred. No. 4.2e-86;
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFGLLCLPWLQEGSAFPTIPLSRFLFDNASRAHRLHQLAFDTYQEF--- 57
DB 1 MATGRTSLLAFGLLCLPWLQEGSAFPTIPLSRFLFDNASRAHRLHQLAFDTYQEF 60
QY 58 -----NPQTSLCFSESIPTPSNRRETOQKSNELELRISILLIQSWLEPVQFLR 105
DB 61 YIPKEQKSYFLQNPQTSLCFSESIPTPSNRRETOQKSNELELRISILLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTQIIFKQTYSKEDTSHND 165
DB 121 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTQIIFKQTYSKEDTSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
DB 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

RESULT 2
SOMA_PANTR
ID SOMA_PANTR STANDARD; PRT; 217 AA.
AC P59756;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1).
GN GH1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
RX [1]
RP SEQUENCE FROM N.A.
RA Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;
RT "Independent duplication of the growth hormone gene in three Anthropoid lineages."
RT Anthropolidean lineages."
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
DB EMBL; AF374232; AAL72284.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR KX Hormone; Pituitary; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 217 BY SIMILARITY.
FT DISULFID 79 191 BY SIMILARITY.
FT DISULFID 208 215 BY SIMILARITY.
SQ SEQUENCE 217 AA; 24843 MW; FEA295EDE0518674 CRC64;

Query Match          97.3%; Score 1018.5; DB 1; Length 217;

```

```

Best Local Similarity 92.2%; Pred. No. 1.5e-85;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFGLLCLPWLQEGSAFPTIPLSRFLFDNASRAHRLHQLAFDTYQEF--- 57
DB 1 MAPGRTSLLAFGLLCLPWLQEGSAFPTIPLSRFLFDNASRAHRLHQLAFDTYQEF 60
QY 58 -----NPQTSLCFSESIPTPSNRRETOQKSNELELRISILLIQSWLEPVQFLR 105
DB 61 YIPKEQKSYFLQNPQTSLCFSESIPTPSNRRETOQKSNELELRISILLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTQIIFKQTYSKEDTSHND 165
DB 121 SVFANSLVYGASDSNVYDLLKDLREGIQTLMGRLEDGSPRTQIIFKQTYSKEDTSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
DB 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

RESULT 3
SOMA_MACMU
ID SOMA_MACMU STANDARD; PRT; 217 AA.
AC P33033;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1).
GN GH1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
NCBI_TaxID=9544;
RX [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94008724; PubMed=8404617;
RA Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
RT "Cloning of four growth hormone/chorionic somatomotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta."
RT Endocrinology 133:1744-1752(1993).
RN [2]
RP SEQUENCE OF 27-217.
RX MEDLINE=86129460; PubMed=3080959;
RA Li C.H., Chung D., Lahm H.W., Stein S.;
RT "The primary structure of monkey pituitary growth hormone."
RA Arch. Biochem. Biophys. 245:287-291(1986).
CC -!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
DB EMBL; L16556; AAA18842.1; -.
DR PIR; I67410; I67410.
DR HSSP; P01241; IAXI.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.

```

DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
 KW Hormone; Pituitary; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 217 SOMATOTROPIN.
 FT DISULFID 79 191 BY SIMILARITY.
 FT DISULFID 208 215 BY SIMILARITY.
 FT CONFLICT 100 100 E -> Q (IN REF. 2).
 FT CONFLICT 179 179 N -> D (IN REF. 2).
 SQ SEQUENCE 217 AA; 24913 MW; 2C5180341EBC46D0 CRC64;

Query Match 93.7%; Score 981.5; DB 1; Length 217;
 Best Local Similarity 88.9%; Pred. No. 3.4e-82;
 Matches 193; Conservative 3; Mismatches 6; Indels 15; Gaps 1;

QY 1 MATGRTSLLALFGLLCLPWLQEGSAFPTPLSRFLFNASIRAHRLHQLAFDITYQEF--- 57
 DB 1 MAAGSRTSLLALFALLCLPWLQEGSAFPTPLSRFLFNAMLRHRLHQLAFDITYQEFEEA 60
 QY 58 -----NPQSLCFSESIPTPSNREETQCKSNLELLRISLLLIQSWLEPVQFLR 105
 DB 61 YIPKEQKYSFLQNPQSLCFSESIPTPSNREETQCKSNLELLRISLLLIQSWLEPVQFLR 120
 QY 106 SVFANSIVYGASDSNVYDLKLEEGITQTLMGRLDGSPTGQIFKQYKFTNSHND 165
 DB 121 SVFANSIVYGTSDYVYDLKLEEGITQTLMGRLDGSPTGQIFKQYKFTNSHND 180
 QY 166 ALLKNYGLLYCFRKMDKVFETFLRIQCRSVEGSCGF 202
 DB 181 ALLKNYGLLYCFRKMDKVFETFLRIQCRSVEGSCGF 217

RESULT 4
 SOM2_PANTR STANDARD; PRT; 217 AA.
 AC PS8757;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Growth hormone variant precursor (GH-V) (Placenta-specific growth hormone) (Growth hormone 2).
 GN GH2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;
 RT "Independent duplication of the growth hormone gene in three Anthropoid lineages."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed in the placenta.
 CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL observation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF374233; AAL72285.1;
 DR InterPro; IPR001400; Somatotropin.
 DR Pfam; PF00103; hormone; 1.
 DR PRINTS; PR00836; SOMATOTROPIN.

DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
 KW Hormone; Placenta; Signal; Glycoprotein.
 FT SIGNAL 1 26
 FT CHAIN 27 217 GROWTH HORMONE VARIANT.
 FT DISULFID 79 191 BY SIMILARITY.
 FT DISULFID 208 215 BY SIMILARITY.
 SQ SEQUENCE 217 AA; 24990 MW; 1592AA429075677DE CRC64;

Query Match 91.3%; Score 955.5; DB 1; Length 217;
 Best Local Similarity 87.1%; Pred. No. 8e-80;
 Matches 189; Conservative 4; Mismatches 9; Indels 15; Gaps 1;

QY 1 MATGRTSLLALFGLLCLPWLQEGSAFPTPLSRFLFNASIRAHRLHQLAFDITYQEF--- 57
 DB 1 MAAGSRTSLLALFGLLCLPWLQEGSAFPTPLSRFLFNAMLRHRLHQLAFDITYQEFEEA 60
 QY 58 -----NPQSLCFSESIPTPSNREETQCKSNLELLRISLLLIQSWLEPVQFLR 105
 DB 61 YILKEQKYSFLQNPQSLCFSESIPTPSNREETQCKSNLELLRISLLLIQSWLEPVQFLR 120
 QY 106 SVFANSIVYGASDSNVYDLKLEEGITQTLMGRLDGSPTGQIFKQYKFTNSHND 165
 DB 121 SVFANSIVYGASDSNVYDLKLEEGITQTLMGRLDGSPTGQIFKQYKFTNSHND 180
 QY 166 ALLKNYGLLYCFRKMDKVFETFLRIQCRSVEGSCGF 202
 DB 181 ALLKNYGLLYCFRKMDKVFETFLRIQCRSVEGSCGF 217

RESULT 5
 SOM2_HUMAN STANDARD; PRT; 217 AA.
 AC P01242; P09587;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Growth hormone variant precursor (GH-V) (Placenta-specific growth hormone) (Growth hormone 2).
 GN GH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=83182010; PubMed=7169009;
 RA Seeburg P.H.;
 RT "The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone."
 RL DNA 1:239-249 (1982).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=88243769; PubMed=3379057;
 RA Cooke N.E., Ray J., Emery J.G., Liebhaber S.A.;
 RT "Two distinct species of human growth hormone-variant mRNA in the human placenta predict the expression of novel growth hormone proteins."
 RL J. Biol. Chem. 263:9001-9006 (1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=89024984; PubMed=2460050;
 RA Igout A., Schippo M.L., Frankenne F., Hennen G.;
 RT "Cloning and nucleotide sequence of placental hGH-V cDNA."
 RL Arch. Int. Physiol. Biochim. 96:63-67 (1988).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89307277; PubMed=2744760;
 RA Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A.,
 RA Gelin R.E., Seeburg P.H.;
 RT "The human growth hormone locus: nucleotide sequence, biology, and evolution."
 RL Genomics 4:479-497 (1989).

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; AF339060; AAK52287.1; -.
 CC InterPro; IPR001400; Somatotropin.
 CC Pfam; PF00103; hormone; 1.
 CC PRINTS; PR00836; SOMATOTROPIN.
 CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
 CC PROSITE; PS00338; SOMATOTROPIN_2; 1.
 CC Hormone; Pituitary; Signal.
 CC KW SIGNAL 1 26 BY SIMILARITY.
 CC FT CHAIN 27 217 SOMATOTROPIN.
 CC FT DISULFID 79 191 BY SIMILARITY.
 CC FT DISULFID 208 215 BY SIMILARITY.
 CC SQ SEQUENCE 217 AA; 24864 MW; 9515289992C529P7 CRC64;

Query Match 86.4%; Score 904.5; DB 1; Length 217;
 Best Local Similarity 82.0%; Pred. No. 3.5e-75;
 Matches 178; Conservative 10; Mismatches 14; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCPWLQEGSAPPTIPLSRLEFDNASLRHRLHQLAFDITYQEF--- 57
 DB 1 MATGSRSTLLAFGLLCPWLQEGSAPPTIPLSRLEFDNASLRHRLHQLAFDITYQEFEEA 60
 QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 105
 DB 61 YIPKEQKSYFLQNPQTSLCFSESIPTPASKKETQOKSNLELLRLISLLLIQSWLEPVQFLR 120
 QY 106 SVFANSIVYGASDNVYDLKLEEGIQTLMGRLDGSPRTGQFFKQTSKFDNNSNDD 165
 DB 121 SVFANSILYGVSDVVEYLKLEEGIQTLMGRLDGSPRTGALFRQTSKFDNINSQND 180
 QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
 DB 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

RESULT 7

SOMA CALJA STANDARD; PRT; 217 AA.
 AC OQGB3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Somatotropin precursor (Growth hormone).
 GN GH1.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callithrix.
 OC NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wallis O.C., Wallis M.;
 RT "Cloning and characterisation of a putative growth hormone encoding
 RL gene from the marmoset (Callithrix jacchus).";
 CC Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Plays an important role in growth control. Its major
 CC role in stimulating body growth is to stimulate the liver and
 CC other tissues to secrete IGF-1. It stimulates both the
 CC differentiation and proliferation of myoblasts. It also stimulates
 CC amino acid uptake and protein synthesis in muscle and other
 CC tissues (by similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; AJ297563; CAC03481.1; -.
 CC HSP; P01241; 1A22.
 CC InterPro; IPR001400; Somatotropin.
 CC Pfam; PF00103; hormone; 1.
 CC PRINTS; PR00836; SOMATOTROPIN.
 CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
 CC PROSITE; PS00338; SOMATOTROPIN_2; 1.
 CC Hormone; Pituitary; Signal.
 CC KW SIGNAL 1 26 BY SIMILARITY.
 CC FT CHAIN 27 217 SOMATOTROPIN.
 CC FT DISULFID 79 191 BY SIMILARITY.
 CC FT DISULFID 208 215 BY SIMILARITY.
 CC SQ SEQUENCE 217 AA; 24959 MW; E102151A12CE6192 CRC64;

Query Match 85.5%; Score 895.5; DB 1; Length 217;
 Best Local Similarity 81.1%; Pred. No. 2.3e-74;
 Matches 176; Conservative 11; Mismatches 15; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCPWLQEGSAPPTIPLSRLEFDNASLRHRLHQLAFDITYQEF--- 57
 DB 1 MAAGSWTSLLAFTLLCPQLREAGAPPTIPLSRLLDNAMLRHRLHQLAFDITYQEFEEA 60
 QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 105
 DB 61 YIPKEQKSYFLQNPQTSLCFSESIPTPASKKETQOKSNLELLRLISLLLIQSWLEPVQFLR 120
 QY 106 SVFANSIVYGASDNVYDLKLEEGIQTLMGRLDGSPRTGQFFKQTSKFDNNSNDD 165
 DB 121 SVFANSILYGVSDVVEYLKLEEGIQTLMGRLDGSPRTGTFPMQYRKFDVNSQND 180
 QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 202
 DB 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSCGF 217

RESULT 8

PLL_HUMAN STANDARD; PRT; 217 AA.
 AC P01243;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lactogen precursor (Choriomammotropin) (Chorionic somatomammotropin).
 GN CSH1 AND CSH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (GENE CSH1).
 RA MEDLINE=85030426; PubMed=6208192;
 RA Selby M.J., Barta A., Baxter J.D., Bell G.I., Eberhardt N.L.;
 RT "Analysis of a major human chorionic somatomammotropin gene. Evidence
 RT for two functional promoter elements.";
 RL J. Biol. Chem. 259:13131-13138(1984).
 RN [2]
 RP SEQUENCE FROM N.A. (GENE CSH2).
 RA MEDLINE=87161235; PubMed=3030680;
 RA Hirt H., Kimelman J., Birnbaum M.J., Chen E.Y., Seeburg P.H.,
 RA Eberhardt N.L., Barta A.;
 RT "The human growth hormone gene locus: structure, evolution, and
 RT allelic variations.";
 RL DNA 6:59-70(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=83160916; PubMed=6300056;
 RA Barrera-Galdana H.A., Seeburg P.H., Saunders G.F.;
 RT "Two structurally different genes produce the same secreted human
 RT placental lactogen hormone.";

RL J. Biol. Chem. 258:3787-3793 (1983).
 RN [4]
 RP SEQUENCE FROM N.A. (GENES CSH1 AND CSH2).
 RX MEDLINE=89307277; PubMed=2744760;
 RA Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
 RA Seeburg P.H.;
 RT "The human growth hormone locus: nucleotide sequence, biology, and
 RT evolution.";
 RL Genomics 4:479-497 (1989).
 RN [5]
 RP SEQUENCE.
 RX MEDLINE=83182010; PubMed=7169009;
 RA Seeburg P.H.;
 RT "The human growth hormone gene family: nucleotide sequences show
 RT recent divergence and predict a new polypeptide hormone.";
 RL DNA 1:239-249 (1982).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [7]
 RP SEQUENCE OF 50-217 FROM N.A.
 RX MEDLINE=78071761; PubMed=593368;
 RA Shine J., Seeburg P.H., Martial J.A., Baxter J.D., Goodman H.M.;
 RT "Construction and analysis of recombinant DNA for human chorionic
 RT somatomammotropin.";
 RL Nature 270:494-499 (1977).
 RN [8]
 RP SEQUENCE OF 27-217.
 RX MEDLINE=73201971; PubMed=4712450;
 RA Li C.H., Dixon J.S., Chung D.;
 RT "Amino acid sequence of human chorionic somatomammotropin.";
 RL Arch. Biochem. Biophys. 155:95-110 (1973).
 RN [9]
 RP SEQUENCE OF 10-217.
 RX MEDLINE=72016313; PubMed=5286363;
 RA Sherwood L.M., Handwerger S., McLaurin W.D., Lanner M.;
 RT "Amino acid sequence of human placental lactogen.";
 RL Nature New Biol. 233:59-61 (1971).
 RN [10]
 RP ERRATUM.
 RA Sherwood L.M., Handwerger S., McLaurin W.D., Lanner M.;
 RL Nature New Biol. 235:164-64 (1972).
 RN [11]
 RP INTERCHAIN DISULFIDE BONDS.
 RX MEDLINE=79173081; PubMed=438159;
 RA Schneider A.B., Kowalski K., Russell J., Sherwood L.M.;
 RT "Identification of the interchain disulfide bonds of dimeric human
 RT placental lactogen.";
 RL J. Biol. Chem. 254:3782-3787 (1979).
 CC -!- FUNCTION: Similar to that of somatotropin.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: The sequence of CSH1 is shown.

CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC
 DR EMBL; V00573; CAA23836.1; -
 DR EMBL; J00289; AAA98747.1; -
 DR EMBL; K02401; AAA52115.1; -
 DR EMBL; M15894; AAA52116.1; -
 DR EMBL; J03071; AAA52551.1; -
 DR EMBL; J00118; AAA98621.1; -
 DR EMBL; BC02717; AAH02717.1; -
 DR EMBL; BC005921; AAH05921.1; -
 DR EMBL; BC020756; AAH020756.1; -
 DR PIR; A26449; A26449.
 DR PIR; C32435; LCHUC.
 DR HSSP; P01241; 1A22.
 DR Genew; HGNC:2440; CSH1.
 DR Genew; HGNC:2441; CSH2.
 DR MIM; 150200; -
 DR GO; GO:0007565; P:pregnancy; TAS.
 DR InterPro; IPR001400; Somatotropin.
 DR Pfam; PF00103; hormone; 1.
 DR PRINTS; PR00836; SOMATOTROPIN.
 DR PROSITE; PS00266; SOMATOTROPIN 1; 1.
 DR PROSITE; PS00338; SOMATOTROPIN 2; 1.
 KW Hormone; Placenta; Multi:gene family; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 217 LACTOGEN.
 FT DISULFID 79 191
 FT DISULFID 208 215
 FT DISULFID 208 208
 FT DISULFID 215 215
 FT VARIANT 3 3
 FT VARIANT 104 105
 FT CONFLICT 84 84
 FT CONFLICT 95 95
 FT CONFLICT 116 116
 FT CONFLICT 134 136
 SQ SEQUENCE 217 AA; 25020 MW; 235B0DC7A713F431 CRC64;
 Query Match 83.3%; Score 872.5; DB 1; Length 217;
 Best Local Similarity 79.3%; Pred. No. 2.9e-72;
 Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;
 QY 1 MATGRTSLLAFGLCLPWLQEGSAFTPIPLSLFDNASLRAHLHQLADPTQGEF--- 57
 Db 1 MAPGRTSLLAFALLCLPWLQEGAGVQTVLSRLFDHAMQAHRAHQALDITYGEFET 60
 QY 58 -----NPTSLCFSESIPTPSNREETQOKSLELRLISLLIQSWLEPQFLR 105
 Db 61 YIPKQKYSFLHDSQTSFCFSDSIPTPSNMEETQOKSLELRLISLLIQSWLEPQFLR 120
 QY 106 SVFANSLVYGASDSNVYDILLKDLERGIOTLMGRLEDGSPRTGQIPKQYKSPFTNSHND 165
 Db 121 SMFANNLYVDTSDSDYHLLKDLBEGIQTLNGLRLEDGSRRTGQILKQYKSPFTNSHND 180
 QY 166 ALLKNYGLYCFRKMDDKVTFLRVQCRSEVSGCGF 202
 Db 181 ALLKNYGLYCFRKMDDKVTFLRVQCRSEVSGCGF 217
 RESULT 9
 ID SOM2 MACMU STANDARD; PRY; 217 AA.
 AC Q07370; Q28494;


```
DR 61 YIEGQYSIQNAQAFCSETIPAPGKDEAQQRSMDWELLRLSLLLIQSWLGPVQLSR 120
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 216 SOMATOTROPIN.
FT DISULFID 78 189 BY SIMILARITY.
FT DISULFID 206 214 BY SIMILARITY.
FT CONFLICT 4 4 S -> G (IN REF. 1).
FT CONFLICT 7 7 N -> T (IN REF. 1).
SQ SEQUENCE 216 AA; 24468 MW; ABAD1DD59FIDAARD CRC64;

Query Match 65.6%; Score 687; DB 1; Length 216;
Best Local Similarity 63.6%; Pred. No. 2.2e-55;
Matches 138; Conservative 20; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAPPTPLSLRFDNASLRHLRHLQLAFTDYQEF--- 57
Db 1 MAASPRNSVLLAFALLCLPWPQEVGAPFAPMPLSSLFANAVLRAQLHLQLAADTYKEPERA 60
QY 58 -----NPQTSLCFSESPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLRS 106
Db 61 YIEGQYSIQNAQAFCSETIPAPGKDEAQQRSMDWELLRLSLLLIQSWLGPVQLSR 120
QY 107 VFANSVYGASDSNVYDLLKDLREGIOTLMGRLEDGSPRTGQIFPKQYSKFDTNSHNDDA 166
Db 121 VFTNSLVFGTSD-RVYEKLRLDLBEGIQALMRELEDGSPRAGQILKQTYDKFDTNLRSDDA 179
QY 167 LLKNYGLLYCFRKDMKVETFLRIVQCRS-VEGSCGF 202
Db 180 LLKNYGLLYCFKDLHLKAEIYLRVMKCRFFVESSCAF 216

RESULT 13
SOMA_FELCA
ID -SOMA_FELCA STANDARD; PRT; 216 AA.
AC P46404;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Somatotropin precursor (Growth hormone).
GN GHI.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary; PubMed=8654953;
RX MEDLINE=96194906;
RA Warren W.C., Bentle K.A., Bogosian G.;
RT "Cloning of the cDNAs coding for cat growth hormone and prolactin.";
RL Gene 168:247-249(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary; PubMed=7642118;
RX MEDLINE=95369713; PubMed=7642118;
RA Castro-Peralta F., Barrera-Saldana H.A.;
RT "Cloning and sequencing of cDNA encoding the cat growth hormone.";
RL Gene 160:311-312(1995).
CC -!- FUNCTION: Plays an important role in growth control. Its major
CC role in stimulating body growth is to stimulate the liver and
CC other tissues to secrete IGF-1. It stimulates both the
CC differentiation and proliferation of myoblasts. It also stimulates
CC amino acid uptake and protein synthesis in muscle and other
CC tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; 223067; CA80601.1; -.
CC EMBL; U92533; AAF21502.1; -.
CC EMBL; AF069071; AAD43366.1; -.
CC PIR; I46145; I46145.
CC HSSP; P01246; 1BST.
CC InterPro; IPR001400; Somatotropin.
CC Pfam; PF00103; hormone; 1.
CC PRINTS; PR00836; SOMATOTROPIN.
CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
```

```
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Hormone; Pituitary; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 216 SOMATOTROPIN.
FT DISULFID 78 189 BY SIMILARITY.
FT DISULFID 206 214 BY SIMILARITY.
FT CONFLICT 4 4 S -> G (IN REF. 1).
FT CONFLICT 7 7 N -> T (IN REF. 1).
SQ SEQUENCE 216 AA; 24468 MW; ABAD1DD59FIDAARD CRC64;

Query Match 65.6%; Score 687; DB 1; Length 216;
Best Local Similarity 63.6%; Pred. No. 2.2e-55;
Matches 138; Conservative 20; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAPPTPLSLRFDNASLRHLRHLQLAFTDYQEF--- 57
Db 1 MAASPRNSVLLAFALLCLPWPQEVGAPFAPMPLSSLFANAVLRAQLHLQLAADTYKEPERA 60
QY 58 -----NPQTSLCFSESPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLRS 106
Db 61 YIEGQYSIQNAQAFCSETIPAPGKDEAQQRSMDWELLRLSLLLIQSWLGPVQLSR 120
QY 107 VFANSVYGASDSNVYDLLKDLREGIOTLMGRLEDGSPRTGQIFPKQYSKFDTNSHNDDA 166
Db 121 VFTNSLVFGTSD-RVYEKLRLDLBEGIQALMRELEDGSPRAGQILKQTYDKFDTNLRSDDA 179
QY 167 LLKNYGLLYCFRKDMKVETFLRIVQCRS-VEGSCGF 202
Db 180 LLKNYGLLYCFKDLHLKAEIYLRVMKCRFFVESSCAF 216

RESULT 13
SOMA_FELCA
ID -SOMA_FELCA STANDARD; PRT; 216 AA.
AC P46404;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Somatotropin precursor (Growth hormone).
GN GHI.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary; PubMed=8654953;
RX MEDLINE=96194906;
RA Warren W.C., Bentle K.A., Bogosian G.;
RT "Cloning of the cDNAs coding for cat growth hormone and prolactin.";
RL Gene 168:247-249(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary; PubMed=7642118;
RX MEDLINE=95369713; PubMed=7642118;
RA Castro-Peralta F., Barrera-Saldana H.A.;
RT "Cloning and sequencing of cDNA encoding the cat growth hormone.";
RL Gene 160:311-312(1995).
CC -!- FUNCTION: Plays an important role in growth control. Its major
CC role in stimulating body growth is to stimulate the liver and
CC other tissues to secrete IGF-1. It stimulates both the
CC differentiation and proliferation of myoblasts. It also stimulates
CC amino acid uptake and protein synthesis in muscle and other
CC tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; 223067; CA80601.1; -.
CC EMBL; U92533; AAF21502.1; -.
CC EMBL; AF069071; AAD43366.1; -.
CC PIR; I46145; I46145.
CC HSSP; P01246; 1BST.
CC InterPro; IPR001400; Somatotropin.
CC Pfam; PF00103; hormone; 1.
CC PRINTS; PR00836; SOMATOTROPIN.
CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
```

```
or send an email to license@isb-sib.ch).
-----
CC CC EMBL; U25973; AAA67294.1; -.
CC CC EMBL; U13390; AAA36142.1; -.
CC DR PIR; JC4632; JC4632.
CC DR HSSP; P01246; 1BST.
CC DR InterPro; IPR001400; Somatotropin.
CC DR Pfam; PF00103; hormone; 1.
CC DR PRINTS; PR00836; SOMATOTROPIN.
CC DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
CC DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
CC KW Hormone; Pituitary; Signal.
CC FT SIGNAL 1 26 BY SIMILARITY.
CC FT CHAIN 27 216 SOMATOTROPIN.
CC FT DISULFID 78 189 BY SIMILARITY.
CC FT DISULFID 206 214 BY SIMILARITY.
CC FT CONFLICT 7 N -> T (IN REF. 2).
CC FT CONFLICT 26 26 T -> A (IN REF. 2).
CC FT CONFLICT 159 159 G -> A (IN REF. 2).
CC FT CONFLICT 181 181 L -> P (IN REF. 2).
CC SQ SEQUENCE 216 AA; 24454 MW; 05820239A7D292C6 CRC64;

Query Match 65.6%; Score 687; DB 1; Length 216;
Best Local Similarity 63.6%; Pred. No. 2.2e-55;
Matches 138; Conservative 20; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATGRTSLLLAFGLICLPWLOEGSAFPTIPISRLFDNASLRAHRLHQLAFDTYQEF--- 57
D 1 MAAGPRNSVLLAFALLCLPWPQEVGTFPAMPPLSSLPANAVLAQAHLHQLAADTYKEFERA 60
QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELRISLLLIQSWLEPVQFLRS 106
D 61 YIPEGQRYSIQNAQAACFCSETIPAPTKEEAQQRSDMELLRFSLLLIQSWLGPVQFLSR 120
QY 107 VFANSIVYGASDSNVYLLKLEEGITQTLMGLEDGSPRTGTFKQTYSKFDTNSHDDA 166
D 121 VFTNSLVFTGSD-RVYEKLKLEEGIQALMRELEDGSPRGQLLKQTYDKFTNLSDDA 179
QY 167 LKKNYGLLYCFRKMDKVETFLRIVQCRS-VEGSGCF 202
D 180 LKKNYGLLSCFKKDLHKAETYLVRMKCRFVSSCAF 216

RESULT 14
SOMA_MESAU STANDARD; PRT; 216 AA.
AC P37886;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Somatotropin precursor (Growth hormone).
GN GH1 OR GH.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92063850; PubMed=1954881;
RA Southard J.N., Sanchez-Jimenez F., Campbell G.T., Talamantes F.;
RT "Sequence and expression of hamster prolactin and growth hormone messenger RNAs."
RL Endocrinology 129:2965-2971(1991).
CC -!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
-----

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
CC CC EMBL; S66299; AAB20368.1; -.
CC CC HSSP; P01246; 1BST.
CC DR InterPro; IPR001400; Somatotropin.
CC DR Pfam; PF00103; hormone; 1.
CC DR PRINTS; PR00836; SOMATOTROPIN.
CC DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
CC DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
CC KW Hormone; Pituitary; Signal.
CC FT SIGNAL 1 26 BY SIMILARITY.
CC FT CHAIN 27 216 SOMATOTROPIN.
CC FT DISULFID 78 189 BY SIMILARITY.
CC FT DISULFID 206 214 BY SIMILARITY.
CC SQ SEQUENCE 216 AA; 24690 MW; 3B69CE32AB6F1166 CRC64;

Query Match 65.1%; Score 682; DB 1; Length 216;
Best Local Similarity 63.1%; Pred. No. 6.2e-55;
Matches 137; Conservative 21; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATGRTSLLLAFGLICLPWLOEGSAFPTIPISRLFDNASLRAHRLHQLAFDTYQEF--- 57
D 1 MAADSQTSLLFTLLCLLPQEQAGAPFAMPPLSSLPANAVLAQAHLHQLAADTYKEFERA 60
QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELRISLLLIQSWLEPVQFLRS 106
D 61 YIPEGQRYSIQNAQAACFCSETIPAPTKEEAQQRSDMELLRFSLLLIQSWLGPVQFLSR 120
QY 107 VFANSIVYGASDSNVYLLKLEEGITQTLMGLEDGSPRTGTFKQTYSKFDTNSHDDA 166
D 121 IFTNSLMFTGSD-RVYEKLKLEEGIQALMQLELEDGSPRVGQILKQTYDKFTNMRSDDA 179
QY 167 LKKNYGLLYCFRKMDKVETFLRIVQCRS-VEGSGCF 202
D 180 LKKNYGLLSCFKKDLHKAETYLVRMKCRFVSSCAF 216

RESULT 15
SOMA_RABIT STANDARD; PRT; 216 AA.
AC P46407;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Somatotropin precursor (Growth hormone).
GN GH1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=New Zealand white;
RX MEDLINE=96011843; PubMed=7590276;
RA Wallis O.C., Wallis M.;
RT "Cloning and characterisation of the rabbit growth hormone-encoding gene."
RL Gene 163:253-256(1995).
CC -!- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
```

```

-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; Z38127; CAA86287.1; -.
DR PIR; S49483; S49483.
DR HSP; P01246; 1BST.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Hormone; Pituitary; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 216 SOMATOTROPIN.
FT DISULFID 78 189 BY SIMILARITY.
FT DISULFID 206 214 BY SIMILARITY.
SQ SEQUENCE 216 AA; 24433 MW; 6EC19748199F9D75 CRC64;

Query Match 65.1%; Score 682; DB 1; Length 216;
Best Local Similarity 63.1%; Pred. No. 6.2e-55;
Matches 137; Conservative 21; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATGSRSLLLAFGLLCLPWLQEGSAFPTTPLSLFDNASLRHRLHQLAPDTYQEP--- 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MAGSWTAGLLAFALLCLPWPQEAFAFPAMPFLSSLFANAVLRAQHQLAADTYKEFERA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 58 -----NPQTSLCFSESITPSNREHTQOKSNLELRISILLIQSWLEPVQFLRS 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YIPEGQRYSIQAQAFCFSETIPATCKDAQQRSDMELLRFSLLLIQSWLGPVQLSR 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 107 VFANSLVYGASDSNVYDILLKDLREGIQTLMGRLEDGSPRTGQIFKQYTSKFDTNSHND 166
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 AFTNVLVFGTSD-RVYEKLDLEGIQALMRELEDGSPRVGQLLKQIVDKFDTNLRGDDA 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 167 LLKNYGLLYCPRKMDKVETFLRIVQCRS-VEGSGCF 202
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 LLKNYGLLSCPKDLHKAETVLRVMKCRRFVSSCVF 216
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: July 12, 2004, 13:04:24
Job time : 18 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:01:07 ; Search time 45 Seconds
(without alignments)
1416.326 Million cell updates/sec

Title: US-09-856-796B-2

Perfect score: 1047

Sequence: 1 MATGRTSLLLAFLGLCLPW.....KVETFLRIVQCRSEVSGSGF 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_rodent:*
- 11: sp_virus:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 957 | 91.4 | 202 | 4 | O14643 homo sapien |
| 2 | 908.5 | 86.8 | 217 | 6 | Q8WNE0 ateles geof |
| 3 | 882.5 | 84.3 | 217 | 6 | Q866U1 pan troglod |
| 4 | 873.5 | 83.4 | 217 | 4 | O14407 homo sapien |
| 5 | 866.5 | 82.8 | 217 | 6 | Q07369 macaca mula |
| 6 | 855.5 | 81.7 | 217 | 6 | Q866T8 pan troglod |
| 7 | 853.5 | 81.5 | 217 | 6 | Q866U0 pan troglod |
| 8 | 850.5 | 81.2 | 217 | 6 | Q07367 macaca mula |
| 9 | 831.5 | 79.4 | 212 | 6 | Q07368 macaca mula |
| 10 | 779.5 | 72.1 | 199 | 4 | O14406 homo sapien |
| 11 | 754.5 | 72.1 | 217 | 6 | Q8WNE0 ateles geof |
| 12 | 751.5 | 71.8 | 217 | 6 | Q8MI74 callithrix |
| 13 | 728.5 | 69.6 | 217 | 6 | Q8MI75 callithrix |
| 14 | 726.5 | 69.4 | 184 | 6 | Q866T9 pan troglod |
| 15 | 702 | 67.0 | 216 | 6 | Q8MI73 delphinus d |
| 16 | 701 | 67.0 | 216 | 6 | Q7YQB8 hippopotamu |

| | | | | | |
|----|-------|------|-----|----|--------|
| 17 | 696 | 66.5 | 216 | 6 | Q7YRR6 |
| 18 | 688 | 65.7 | 216 | 11 | O70615 |
| 19 | 681 | 65.0 | 217 | 6 | Q28957 |
| 20 | 678 | 64.8 | 217 | 6 | Q7YQD2 |
| 21 | 677 | 64.7 | 217 | 6 | Q864S7 |
| 22 | 673.5 | 64.3 | 167 | 4 | F78451 |
| 23 | 673 | 64.3 | 216 | 11 | Q9R2C3 |
| 24 | 672 | 64.2 | 216 | 6 | Q8HYE5 |
| 25 | 671 | 64.1 | 216 | 11 | Q9JKM4 |
| 26 | 670 | 64.0 | 217 | 6 | Q9BEB9 |
| 27 | 665 | 63.5 | 217 | 6 | Q9BEC0 |
| 28 | 620 | 59.2 | 204 | 6 | Q9S205 |
| 29 | 608.5 | 58.1 | 245 | 4 | O14644 |
| 30 | 591 | 56.4 | 190 | 11 | Q9JKG0 |
| 31 | 590 | 56.4 | 192 | 6 | Q9TU21 |
| 32 | 589 | 56.3 | 192 | 6 | Q9TOW9 |
| 33 | 554 | 52.9 | 216 | 13 | Q804M1 |
| 34 | 539 | 51.5 | 128 | 4 | Q8NHT7 |
| 35 | 536 | 51.2 | 217 | 13 | Q7TIC3 |
| 36 | 526.5 | 50.3 | 178 | 6 | Q95MJ6 |
| 37 | 516.5 | 49.3 | 176 | 6 | Q95MJ5 |
| 38 | 516 | 49.3 | 218 | 13 | Q9PU72 |
| 39 | 466.5 | 44.6 | 215 | 13 | Q7ZU47 |
| 40 | 465 | 44.4 | 195 | 13 | Q91386 |
| 41 | 449 | 42.9 | 128 | 11 | Q8BK24 |
| 42 | 448.5 | 42.8 | 145 | 6 | Q9BDR4 |
| 43 | 442.5 | 42.3 | 143 | 6 | Q95240 |
| 44 | 415 | 39.6 | 120 | 6 | Q9TSG0 |
| 45 | 394.5 | 37.7 | 209 | 13 | Q8AXX9 |

ALIGNMENTS

RESULT 1

O14643 PRELIMINARY; PRT; 202 AA.
AC O14643; TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Placental growth hormone 20kDa isoform precursor.
GN HGH-V.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Term placenta;
RX MEDLINE=98373737; PubMed=9709963;
RA Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,
RA Carlsson L.M.S., Carlsson B.;
RT "Cloning of two novel growth hormone transcripts expressed in human
RT placenta.";
RL J. Clin. Endocrinol. Metab. 83:2878-2885(1998).
DR EMEL; AF006060; AAB71828.1; -.
DR HSSP; P01241; 1A22.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Signal.
FT SIGNAL. 1 26 POTENTIAL.
SQ SEQUENCE 202 AA; 23128 MW; 38B64D011A9197C6 CRC64;

Query Match 91.4%; Score 957; DB 4; Length 202;

Best Local Similarity 92.6%; Pred. No. 4.6e-83;

Matches 187; Conservative 4; Mismatches 11; Indels 0; Gaps 0;


```

RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; J03071; AA52553.1; -.
DR EMBL; BC022044; AAH22044.1; -.
DR EMBL; BC035965; AAH35965.1; -.
DR PIR; E32435; E32435.
DR HSSP; P01241; 1A22.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 217 AA; 24994 MW; 39FAACDD6B2E951 CRC64;

Query Match
Best Local Similarity 79.3%; DB 4; Length 217;
Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFGLLCLPWLQEGAVQTVPLSRLEDFHAMLQAHRAHQLAIDITYQEFEE 60
QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 105
DB 61 YIPKOKYSLFHDSDYHLLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 120
QY 106 SVFANSLVYGASDSNVYDLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 165
DB 121 SMFANNLVYDTSDDYHLLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 180
QY 166 ALLKNYGLLYCFRKMDKVKETFLRIVQCRSVEGSCGF 202
DB 181 ALLKNYGLLYCFRKMDKVKETFLRMVQCRSVEGSCGF 217

RESULT 5
Q07369
ID Q07369 PRELIMINARY; PRT; 217 AA.
AC Q07369;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Chorionic somatomammotropin-3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=Midpregnancy placenta;
RX MEDLINE=94008724; PubMed=8404617;
RA Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
RT Cloning of four growth hormone/chorionic somatomammotropin-related
RT complementary deoxyribonucleic acids differentially expressed during
RT pregnancy in the rhesus monkey placenta.;
RL Endocrinology 133:1744-1752 (1993).
DR EMBL; L16554; AAA18841.1; -.
DR PIR; I67409; I67409.
DR HSSP; P01241; 1AXI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 217 AA; 24874 MW; F1EB6AFDBB185 CRC64;

Query Match
Best Local Similarity 82.8%; Score 866.5; DB 6; Length 217;
Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;

RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; J03071; AA52553.1; -.
DR EMBL; BC022044; AAH22044.1; -.
DR EMBL; BC035965; AAH35965.1; -.
DR PIR; E32435; E32435.
DR HSSP; P01241; 1A22.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 217 AA; 24994 MW; 39FAACDD6B2E951 CRC64;

Query Match
Best Local Similarity 79.3%; DB 4; Length 217;
Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFGLLCLPWLQEGAVQTVPLSRLEDFHAMLQAHRAHQLAIDITYQEFEE 60
QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 105
DB 61 YIPKOKYSLFHDSDYHLLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 120
QY 106 SVFANSLVYGASDSNVYDLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 165
DB 121 SMFANNLVYDTSDDYHLLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 180
QY 166 ALLKNYGLLYCFRKMDKVKETFLRIVQCRSVEGSCGF 202
DB 181 ALLKNYGLLYCFRKMDKVKETFLRMVQCRSVEGSCGF 217

RESULT 6
Q866T8
ID Q866T8 PRELIMINARY; PRT; 217 AA.
AC Q866T8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Placental lactogen PL-D.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Revol A., Esquivel D.E., Barrera H.S.;
RT "The GH-PL locus a hot-point between human and chimpanzee genomes.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY146628; AAN84508.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 217 AA; 25135 MW; 1EB7B98B8A12B4F4 CRC64;

Query Match
Best Local Similarity 81.7%; Score 855.5; DB 6; Length 217;
Matches 169; Conservative 12; Mismatches 21; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAPGSRSTLLAFGLLCLPWLQEGAVQTVPLSRLEDFHAMLQAHRAHQLAIDITYQEFEE 60
QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 105
DB 61 YIPKOKYSLFHDSDYHLLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 120
QY 106 SVFANSLVYGASDSNVYDLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 165
DB 121 SMFANNLVYDTSDDYHLLKOLEGIQTLMRLEDSGSRPTGQIFKQYTSKFDNTSHND 180
QY 166 ALLKNYGLLYCFRKMDKVKETFLRIVQCRSVEGSCGF 202
DB 181 ELLKNYGLLYCFRKMDKVKETFLRMVQCRSVEGSCGF 217

RESULT 7
Q866U0
ID Q866U0 PRELIMINARY; PRT; 217 AA.
AC Q866U0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

```

```
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Placental lactogen PL-B.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
CX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Revol A., Esquivel D.E., Barrera H.S.;
RT "The GH-PL locus a hot-point between human and chimpanzee genomes.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY146626; AAN84506.1; -.
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0005179; F:hormone activity; IEA.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 217 AA; 24884 MW; A1663257499827D4 CRC64;

Query Match 81.5%; Score 853.5; DB 6; Length 217;
Best Local Similarity 77.9%; Pred. No. 3.7e-73;
Matches 169; Conservative 11; Mismatches 22; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFALLCLPWLQEGAGVQTVPLSLFKKAMLQAPAHQLAIDITYQEFEEA 60
QY 58 -----NPQSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 105
DB 61 YIPKQKYSLHDSQTSFCSDSIPTPSNMEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 106 SVFANSIVYGASDNVYDLKDLLEGITQTLMGRLDGSPTGQIFKQYKFDNSHND 165
DB 61 YIPKQKYSLHDSQTSFCSDSIPTPSNMEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 121 SMFANNLVYDTSDDYHLLKDLLEGITQTLMGRLDGSPTGQILKQYKFDNSHND 180
QY 166 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 202
DB 181 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 217

Query Match 81.5%; Score 853.5; DB 6; Length 217;
Best Local Similarity 77.9%; Pred. No. 3.7e-73;
Matches 169; Conservative 11; Mismatches 22; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFALLCLPWLQEGAGVQTVPLSLFKKAMLQAPAHQLAIDITYQEFEEA 60
QY 58 -----NPQSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 105
DB 61 YIPKQKYSLHDSQTSFCSDSIPTPSNMEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 106 SVFANSIVYGASDNVYDLKDLLEGITQTLMGRLDGSPTGQIFKQYKFDNSHND 165
DB 61 YIPKQKYSLHDSQTSFCSDSIPTPSNMEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 121 SMFANNLVYDTSDDYHLLKDLLEGITQTLMGRLDGSPTGQILKQYKFDNSHND 180
QY 166 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 202
DB 181 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 217

Query Match 81.5%; Score 853.5; DB 6; Length 217;
Best Local Similarity 77.9%; Pred. No. 3.7e-73;
Matches 169; Conservative 11; Mismatches 22; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFALLCLPWLQEGAGVQTVPLSLFKKAMLQAPAHQLAIDITYQEFEEA 60
QY 58 -----NPQSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 105
DB 61 YIPKQKYSLHDSQTSFCSDSIPTPSNMEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 106 SVFANSIVYGASDNVYDLKDLLEGITQTLMGRLDGSPTGQIFKQYKFDNSHND 165
DB 61 YIPKQKYSLHDSQTSFCSDSIPTPSNMEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 121 SMFANNLVYDTSDDYHLLKDLLEGITQTLMGRLDGSPTGQILKQYKFDNSHND 180
QY 166 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 202
DB 181 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 217
```

```
SQ SEQUENCE 217 AA; 24942 MW; FF5AA8915131F2BC CRC64;

Query Match 81.2%; Score 850.5; DB 6; Length 217;
Best Local Similarity 75.6%; Pred. No. 7.1e-73;
Matches 164; Conservative 18; Mismatches 20; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDITYQEF--- 57
DB 1 MAAGSRSTLLAFALLCLPWLQEGAGVQTVPLSLFKKAMLQAPAHQLAIDITYQEFEEA 60
QY 58 -----NPQSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 105
DB 61 YIPKQKYSLHDSQTSFCSDSIPTPSNMEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 106 SVFANSIVYGASDNVYDLKDLLEGITQTLMGRLDGSPTGQIFKQYKFDNSHND 165
DB 121 SVFANNLLHHTSDSDVHLLKDLLEGITQTLMGRLDGSPTGQIFKQYKFDNSHND 180
QY 166 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 202
DB 181 SLLKNYGLLYCFRDKMDKVETFLRIVQCRSVGSGCF 217

RESULT 9
Q07368 PRELIMINARY; PRT; 212 AA.
ID Q07368
AC Q07368;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Somatotropin 2 precursor (Growth hormone 2) (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94008724; PubMed=8404617;
RA Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
RT "Cloning of four growth hormone/chorionic somatomotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
RL Endocrinology 133:1744-1752(1993).
DR EMBL: L16553; AAA18840.1; -.
DR PIR: I67408; I67408.
DR HSSP; P01241; IAXI.
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0005179; F:hormone activity; IEA.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
FT NON TER 1
SQ SEQUENCE 212 AA; 24525 MW; 27BC91106256E6F5 CRC64;

Query Match 79.4%; Score 831.5; DB 6; Length 212;
Best Local Similarity 75.5%; Pred. No. 4.4e-71;
Matches 160; Conservative 18; Mismatches 19; Indels 15; Gaps 1;

QY 6 RTSLLAFGLLCLPWLQEGSAFPTIPLSRLFDNASLRAHRLHQLAFDITYQEF----- 57
DB 1 RTSLLAFGLLCLPWLQEGAGVQTVPLSLFKKAMLQAPAHQLAIDITYQEFEEA 60
QY 58 -----NPQSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPQVFLR 110
DB 61 KKHSLMENPQASFCFADSIPTSPNLEETQOKSNLELLRISLLLIQSWLEPQVFLR 120
QY 111 SLVYGASDNVYDLKDLLEGITQTLMGRLDGSPTGQIFKQYKFDNSHND 170
DB 121 NLLHHTSDSDVHLLKDLLEGITQTLMGRLDGSPTGQIFKQYKFDNSHND 180
```



```
QY 171 YGLLYCFKMDKVKVETFLRVQCRVSGSGF 202
DB 181 YGLLHCFKMDKVKVETFLRVQCRVSGSGF 212

RESULT 10
Q14406
ID Q14406 PRELIMINARY; PRT; 199 AA.
AC Q14406;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Chorionic somatomammotropin CS-5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89307277; PubMed=2744760;
RA Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
RA Seeburg P.H.;
RT "The human growth hormone locus: nucleotide sequence, biology, and
RT evolution."
RL Genomics 4:479-497 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91102558; PubMed=1980158;
RA Vnencak-Jones C.L., Phillips J.A. III.;
RT "Hot spots for growth hormone gene deletions in homologous regions
RT outside of Alu repeats."
RL Science 250:1745-1748 (1990).
DR EMBL; J03071; AAA52550.1; -.
DR PIR; B32435; B32435.
DR HSSP; P01241; 1A22.
DR Genew; HGNC:2442; CSHL1.
DR GO; GO:0005179; F: hormone activity; NAS.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR SEQUENCE 199 AA; 22649 MW; 119656E87AFD55C3 CRC64;

Query Match 74.5%; Score 779.5; DB 4; Length 199;
Best Local Similarity 77.7%; Pred. No. 3.7e-66;
Matches 157; Conservative 10; Mismatches 32; Indels 3; Gaps 1;

QY 1 MATGRTSLLAFGLLCLPWLQEGSAFTPIPLSRFLDNASLRAHRLHQLAFDTYQEFNPQ 60
DB 1 MAAGRTSLLAFGLLCLPWLQEGAVQTVPLSRFLDKAMQLQAHRAHQLAIDTYQEFISS 60

QY 61 TSLCFSESIPTPSNREETQOKSNLELLRISLLIQSWLEPVQFLRSVFANSVYGASDSN 120
DB 61 WGM---DSIPTSSNMEETQOKSNLELLRISLLIESRLPEVRFLESTFTNNLVYDTSDD 117

QY 121 VYDLKDLKEEGTQTLMGLEDGSPRTGQIFKQTYSKFDTNSHNDALLKNYGLLYCFRKD 180
DB 118 DYHLKDLKEEGTQTLMGLEDGSHLTGQTLKQTYSKFDTNSHNDALLKNYGLLYCFRKD 177

QY 181 MDKVETFLRVQCRVSGSGF 202
DB 178 MDKVETFLRVQCRVSGSGF 199

RESULT 11
Q8WND9
ID Q8WND9 PRELIMINARY; PRT; 217 AA.
AC Q8WND9;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Growth hormone.
GN GH-V.

Query Match 71.8%; Score 751.5; DB 6; Length 217;
Best Local Similarity 69.1%; Pred. No. 9.8e-64;
Matches 150; Conservative 18; Mismatches 34; Indels 15; Gaps 1;
```

```
OS Ateles geoffroyi (Black-handed spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
OX NCBI_TaxID=9509;
RN [1]
RP SEQUENCE FROM N.A.
RA Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;
RT "Independent duplication of the growth hormone gene in three
RT Anthropoid lineages."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF374235; AAL72287.1; -.
DR GO; GO:0005576; C: extracellular; IEA.
DR GO; GO:0005179; F: hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
DR SEQUENCE 217 AA; 25293 MW; 741745A1B75C053E CRC64;

Query Match 72.1%; Score 754.5; DB 6; Length 217;
Best Local Similarity 69.1%; Pred. No. 9.8e-64;
Matches 150; Conservative 18; Mismatches 34; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFGLLCLPWLQEGSAFTPIPLSRFLDNASLRAHRLHQLAFDTYQEF--- 57
DB 1 MAAGSRMSLLTLLALLCLPWLQETGAFPRIPLSRLFGDAMLRHQHQAFTDYQELEEN 60

QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLIQSWLEPVQFLR 105
DB 61 CIPKQKQVFFLRNPKNFCFSESIPTPNKEVLAQSLLELHLSLLIQSWLEPVQFLR 120

QY 106 SVFANSVYGASDSNVYDLKDLKEEGTQTLMGLEDGSPRTGQIFKQTYSKFDTNSHND 165
DB 121 GVFNQSRHNISNTDVEYVLEKLEGIQLTWLEDGSPQTGEIFRQTYKFKDRSHND 180

QY 166 ALLKNYGLLYCFRKMDKVKVETFLRVQCRVSGSGF 202
DB 181 ALLKNYGLLYCFRKMDKVKVETFLRVQCRVSGSGF 217

RESULT 12
Q8MI74
ID Q8MI74 PRELIMINARY; PRT; 217 AA.
AC Q8MI74;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Growth hormone-like protein 6 precursor.
GN GHUP6.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Wallis O.C., Wallis M.;
RT "Characterisation of the GH gene cluster in a new-world monkey, the
RT marmoset (Callithrix jacchus).";
RL J. Mol. Endocrinol. 0:0-0 (2002).
DR EMBL; AJ489811; CAD34012.1; -.
DR GO; GO:0005576; C: extracellular; IEA.
DR GO; GO:0005179; F: hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW SIGNAL.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 217 GROWTH HORMONE-LIKE PROTEIN 6.
FT SEQUENCE 217 AA; 25177 MW; 5ECF148798278F1A CRC64;

Query Match 71.8%; Score 751.5; DB 6; Length 217;
```

```

Best Local Similarity 67.7%; Pred. No. 1.9e-63;
Matches 147; Conservative 23; Mismatches 32; Indels 15; Gaps 1;

Qy 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFLDNASLRHRLHQLAFDTYQEP--- 57
Db 1 MAAGSRSLMLAFALLCLPWLQETGALPIPLSRFLDGLAMLRARQLHHLALETYREFEKN 60
Qy 58 -----NPQTSICFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105
Db 61 CVPKEQKYFLRNPETVCFSESIPTPFHKEMLGKSNVELLHLSLLLIQSWLEPMQRLG 120
Qy 106 SVFANSILVYGASDSNVYDLKDLKEGIQTLGRLEDGSPRTGQIFKQYTSKFDNNSHND 165
Db 121 SIFANSQHLSTVNTDVEYLKDLKEGIQTLGRLEDGSPQGEIFRQYTSKFDNNSHND 180
Qy 166 ALLKNYGLLYCFRKMDKVFTRIVQCRSVGSGCF 202
Db 181 TLLKNYWLLECFRKDMKVKVTFRLIVQCHSVGSGCF 217

RESULT 13
Q8MI75 PRELIMINARY; PRT; 217 AA.
AC Q8MI75;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Growth hormone-like protein 5 precursor.
GN GHLPS.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Wallis O.C., Wallis M.;
RT "Characterisation of the GH gene cluster in a new-world monkey, the
marmoset (Callithrix jacchus).";
RL J. Mol. Endocrinol. 0:0-0(2002).
DR EMBL; AJ489810; CAB34011.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Signal.
FT SIGNAL
FT CHAIN
FT SEQUENCE 217 AA; 25020 MW; E53419A76C87303F CRC64;

Query Match 69.6%; Score 728.5; DB 6; Length 217;
Best Local Similarity 66.7%; Pred. No. 2.9e-61;
Matches 144; Conservative 25; Mismatches 32; Indels 15; Gaps 1;

Qy 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFLDNASLRHRLHQLAFDTYQ----- 55
Db 1 MAAVSPASLLLTFTLLCLPWLREAGAQSIPLSSLYDVAVIRAYRLNHLAFDIYQKPEEA 60
Qy 56 -----EFNPQTSICFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105
Db 61 RSPKEQKNFFQFNARTSLCFSSASVPTPNRKTTLQKSNLELLQNSLLLIQWLKPMQSLN 120
Qy 106 SVFANSILVYGASDSNVYDLKDLKEGIQTLGRLEDGSPRTGQIFKQYTSKFDNNSHND 165
Db 121 SVFANSQHSVNSNFIYELKDLKEVIQTLGRLEDGSPWTCGEIFRQYTSKFDNNSHND 180
Qy 166 ALLKNYGLLYCFRKMDKVFTRIVQCRSVGSGC 201
Db 181 AVLKNYGLLYCFRKDMKVKVTFRLIVKRAVEGSGC 216

RESULT 14

```

```

Q866T9 PRELIMINARY; PRT; 184 AA.
AC Q866T9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Placental lactogen PL-C (Fragment).
DE Pan troglodytes (Chimpanzee).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Revol A., Esquivel D.E., Barrera H.S.;
RT "The GH-PL locus a hot-point between human and chimpanzee genomes.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY146627; AAN84507.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
FT NON TER 184
FT SEQUENCE 184 AA; 21145 MW; 68D1FF4AE59178DD CRC64;

Query Match 69.4%; Score 726.5; DB 6; Length 184;
Best Local Similarity 79.3%; Pred. No. 3.7e-61;
Matches 146; Conservative 9; Mismatches 14; Indels 15; Gaps 1;

Qy 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFLDNASLRHRLHQLAFDTYQEP--- 57
Db 1 MAPGSRSTLLAFGLLCLPWLQEGSAFPTIPLSRFLDNASLRHRLHQLAFDTYQEPFEEA 60
Qy 58 -----NPQTSICFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105
Db 61 YIPKQKYQFSLHDSQTSFCFSDSLTPSNMEETOQKSNLELRISLLLIQSWLEPVQFLR 120
Qy 106 SVFANSILVYGASDSNVYDLKDLKEGIQTLGRLEDGSPRTGQIFKQYTSKFDNNSHND 165
Db 121 SFANNLVYDTSDDYHLKDLKEGIQTLGRLEDGSRRTGQILKQYTSKFDNNSHND 180
Qy 166 ALK 169
Db 181 ALK 184

RESULT 15
Q8MI73 PRELIMINARY; PRT; 216 AA.
AC Q8MI73;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Growth hormone precursor.
OS Delphinus delphis (Saddleback dolphin) (Black sea dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Delphinus.
OX NCBI_TaxID=9728;
RN [1]
RP SEQUENCE FROM N.A.
RA Manion Z., Wallis O.C., Wallis M.;
RT "Cloning and characterisation of the GH gene from the common dolphin
(Delphinus delphis).";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ492191; CAD37292.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.

```

```

DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Signal.
FT SIGNAL. 1 26 POTENTIAL.
FT CHAIN 27 216 GROWTH HORMONE.
SQ SEQUENCE 216 AA; 24509 MW; 1EC467A84CCFEB02 CRC64;

Query Match 67.0%; Score 702; DB 6; Length 216;
Best Local Similarity 64.5%; Pred. No. 9.8e-59;
Matches 140; Conservative 20; Mismatches 41; Indels 16; Gaps 3;

Qy 1 MATGSR TSLILA FGLLCPLWQEGSAPPTPLSLKLPDNASLRHRLHQLAFDTYQEF--- 57
Db 1 MAAGPRT SMLLAFALLCPLWQEVGAPFAPMPLSSLFANAVLRAQHLHQLAADTYKEPERA 60
Qy 58 -----NPQTSLCFSESITPTPSNRSETQOKSNLELLRLISLLIQSLWLEPVQFLRS 106
Db 61 YIEPGQRYSTQNTQAFCFSETTIPAPTKGDEAQQRSDELLRFSLLLIQSLWGPVQFLSR 120
Qy 107 VFANSLVYGASDSNVYDILLKDEEGIO TLMGRLEDGSPRTGQIQPKQYKSFDTNSHNDDA 166
Db 121 VFTNSLVFGTSD-RVYEKLXDEEGIQALMRELEDGSPRAGQILKQTYKEDFTNWRSDDA 179
Qy 167 LKNYGLLYCFRKMDKVFETFLRIVQCRS-VEGSCGF 202
Db 180 LKNYGLLSCFKKDLHKAEITYLRVMKCRRFVESSCAF 216

```

Search completed: July 12, 2004, 13:05:22
Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2004, 12:57:07 ; Search time 61 Seconds
(without alignments)
935.649 Million cell updates/sec

Title: US-09-856-796b-2

Perfect score: 1047

Sequence: 1 MATGSRTSLLLAFLGLCLPW.....KVETFLRIVQCRSVGSGCF 202

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
|------------|--------|-------|--------|----|-----------|--------------------|
| 1 | 1047 | 100.0 | 202 | 3 | AAY93637 | Aay93637 Amino aci |
| 2 | 1029.5 | 98.3 | 217 | 2 | AAR60516 | Aar60516 Human som |
| 3 | 1029.5 | 98.3 | 217 | 5 | AAU11731 | Aau11731 Growth ho |
| 4 | 1029.5 | 98.3 | 217 | 5 | AAU11719 | Aau11719 Growth ho |
| 5 | 1029.5 | 98.3 | 217 | 5 | AAU11720 | Aau11720 Growth ho |
| 6 | 1029.5 | 98.3 | 217 | 5 | AAU11730 | Aau11730 Growth ho |
| 7 | 1029.5 | 98.3 | 217 | 5 | ABG60633 | Abg60633 Human gro |
| 8 | 1028.5 | 98.2 | 217 | 5 | AAU11742 | Aau11742 Growth ho |
| 9 | 1028.5 | 98.2 | 217 | 5 | AAU11726 | Aau11726 Growth ho |
| 10 | 1026.5 | 98.0 | 217 | 5 | AAU11746 | Aau11746 Growth ho |
| 11 | 1025.5 | 97.9 | 217 | 5 | AAU11747 | Aau11747 Growth ho |
| 12 | 1025.5 | 97.9 | 217 | 5 | AAU11735 | Aau11735 Growth ho |
| 13 | 1025.5 | 97.9 | 217 | 5 | AAU11744 | Aau11744 Growth ho |
| 14 | 1025.5 | 97.9 | 217 | 5 | AAU11722 | Aau11722 Growth ho |
| 15 | 1025.5 | 97.9 | 217 | 5 | AAU11728 | Aau11728 Growth ho |
| 16 | 1024.5 | 97.9 | 217 | 2 | AAR05169 | Aar05169 Human gro |
| 17 | 1024.5 | 97.9 | 217 | 3 | AAB26769 | Aab26769 Secretary |
| 18 | 1024.5 | 97.9 | 217 | 4 | AAO17479 | Aao17479 Human gro |
| 19 | 1024.5 | 97.9 | 217 | 4 | AAAB35428 | Aab35428 Secretary |
| 20 | 1024.5 | 97.9 | 217 | 5 | AAU11741 | Aau11741 Growth ho |
| 21 | 1024.5 | 97.9 | 217 | 5 | AAU11727 | Aau11727 Growth ho |
| 22 | 1024.5 | 97.9 | 217 | 5 | AAU11748 | Aau11748 Growth ho |
| 23 | 1024.5 | 97.9 | 217 | 5 | AAU11736 | Aau11736 Growth ho |
| 24 | 1024.5 | 97.9 | 217 | 5 | AAU11750 | Aau11750 Growth ho |
| 25 | 1024.5 | 97.9 | 217 | 5 | AAU11743 | Aau11743 Growth ho |

ALIGNMENTS

RESULT 1
AAY93637
ID AAY93637 standard; protein; 202 AA.

XX AAY93637;
AC AAY93637;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of a human growth hormone (hGH).
XX
KW Human; growth hormone; hGH; inhibitor; nuclear factor-kappaB; NF-kappaB;
KW multi-drug resistance gene; malignant hemopathy; solid tumour;
KW malignant blood disease; leukaemia; lymphoma; solid cancer.
XX
OS Homo sapiens.
XX
PN WO200030587-A2.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-FR002897.
XX
PR 25-NOV-1998; 98FR-00014858.
XX (CNRS) CENT NAT RECH SCI.
XX
PI Hirsch F, Haeffner A;
XX
DR WPI, 2000-399901/34.
DR N-PSDB; AAA46696.
XX
PT Treatment of hematological or solid tumors using an inhibitor of the
PT activation of nuclear factor-kappaB, particularly to prevent development
XX of resistance to chemotherapeutics.
PS Claim 10; Page 27-28; 30pp; French.
XX
CC The present sequence represents a human growth hormone (hGH). The human
CC growth hormone protein is used as an inhibitor of the activation of
CC nuclear factor-kappaB (NF-kappaB). The inhibitor inhibits activation of
CC NF-kappaB, and thus transcription of the multi-drug resistance gene
CC (which contains binding sites for NF-kappaB within its regulatory
CC regions). The inhibitors are used to produce pharmaceuticals which may be
CC used in the treatment of malignant hemopathy or solid tumours. The
CC inhibitors are especially used to treat malignant blood diseases
CC (leukaemia, lymphoma) and solid cancers (of breast or ovary)
XX
SQ Sequence 202 AA;

| | | | | | | |
|----|--------|------|-----|---|-----------|--------------------|
| 26 | 1024.5 | 97.9 | 217 | 5 | AAU11740 | Aau11740 Growth ho |
| 27 | 1024.5 | 97.9 | 217 | 5 | AAU11721 | Aau11721 Growth ho |
| 28 | 1024.5 | 97.9 | 217 | 5 | AAO19993 | Aao19993 Protein o |
| 29 | 1024.5 | 97.9 | 217 | 6 | ABR42662 | Abr42662 Human gro |
| 30 | 1024.5 | 97.9 | 217 | 7 | AAO29552 | Aao29552 Human gro |
| 31 | 1024.5 | 97.9 | 217 | 4 | ADB49195 | Adb49195 Human gro |
| 32 | 1024.5 | 97.9 | 407 | 4 | AAAB49195 | Aab49195 Human gro |
| 33 | 1023.5 | 97.8 | 217 | 5 | AAU11725 | Aau11725 Growth ho |
| 34 | 1023.5 | 97.8 | 217 | 5 | AAU11734 | Aau11734 Growth ho |
| 35 | 1022.5 | 97.7 | 217 | 5 | AAU11738 | Aau11738 Growth ho |
| 36 | 1022.5 | 97.7 | 217 | 5 | AAU11739 | Aau11739 Growth ho |
| 37 | 1022.5 | 97.7 | 217 | 5 | AAU11723 | Aau11723 Growth ho |
| 38 | 1022.5 | 97.7 | 217 | 5 | AAU11724 | Aau11724 Growth ho |
| 39 | 1022.5 | 97.7 | 217 | 5 | AAU11745 | Aau11745 Growth ho |
| 40 | 1022.5 | 97.7 | 217 | 5 | AAU11901 | Aau11901 Growth ho |
| 41 | 1022.5 | 97.7 | 217 | 5 | AAU11733 | Aau11733 Growth ho |
| 42 | 1021.5 | 97.6 | 217 | 5 | AAU11749 | Aau11749 Growth ho |
| 43 | 1021.5 | 97.6 | 217 | 6 | ABR42665 | Abr42665 Human gro |
| 44 | 1020.5 | 97.5 | 217 | 5 | AAU11729 | Aau11729 Growth ho |
| 45 | 1019.5 | 97.4 | 217 | 6 | ABR42666 | Abr42666 Human gro |

| | | | | |
|--|-----------------|------------------|------------------|------------------------------------|
| Query Match | 100.0%; | Score 1047; | DB 3; | Length 202; |
| Best Local Similarity | 100.0%; | Pred. No. 2e-89; | 0; | Gaps 0; |
| Matches 202; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| 1 MATGSR | TSL | LLAFGLLCLF | PWLQEGSAFPTIPLSR | LFDNASLRAHRLHQLAFDTYQEFNPQ 60 |
| 1 MATGSR | TSL | LLAFGLLCLF | PWLQEGSAFPTIPLSR | LFDNASLRAHRLHQLAFDTYQEFNPQ 60 |
| 61 TSLC | SES | IPTPSNRE | ETQCKSNLELLRIS | ILLIOSWLEPYQFLRSVFANSIVYGASDSN 120 |
| 61 TSLC | SES | IPTPSNRE | ETQCKSNLELLRIS | ILLIOSWLEPYQFLRSVFANSIVYGASDSN 120 |
| 121 VYDL | LKDL | EEGIQTL | MGRLEDGSPRTGQIF | KQTYGKFDTNSHDDALLKNYGLLYCFRKD 180 |
| 121 VYDL | LKDL | EEGIQTL | MGRLEDGSPRTGQIF | KQTYGKFDTNSHDDALLKNYGLLYCFRKD 180 |
| 181 MDKV | ETFLRIVQ | CRSVEG | SCGF 202 | |
| 181 MDKV | ETFLRIVQ | CRSVEG | SCGF 202 | |
| RESULT 2 | | | | |
| AAAR60516 | | | | |
| AAAR60516 | | | | |
| AAAR60516 | | | | |
| 25-MAR-2003 | | | | |
| 22-MAR-1995 | | | | |
| Human somatotropin. | | | | |
| Serine protease; Factor-Xa; recognition site; fusion protein cleavage; | | | | |
| protein folding; growth hormone; somatotropin; primer; | | | | |
| polymerase chain reaction; amplification. | | | | |
| Homo sapiens. | | | | |
| WO9418227-A2. | | | | |
| 18-AUG-1994. | | | | |
| 04-FEB-1994; | | | | |
| 04-FEB-1993; | | | | |
| 05-FEB-1993; | | | | |
| 03-DEC-1993; | | | | |
| (DENZ-) DENZTME APS. | | | | |
| Thogersen HC, Holtet TL, Etzerodt M; | | | | |
| WPI; 1994-279681/34. | | | | |
| Refolding of polypeptide molecules - using a cyclic process involving | | | | |
| denaturing and renaturing conditions to produce a correctly folded prod. | | | | |
| Disclosure; Page 129-30; 202pp; English. | | | | |
| cDNA encoding human somatotropin (aa sequence given in AAR60516) was PCR | | | | |
| amplified using primers given in AA071248-49. Amplified cDNA was linked | | | | |
| to a sequence encoding the Factor-Xa cleavage site (given in AAR60503), | | | | |
| subcloned in vector pTH6 so that it was N-terminally linked to a | | | | |
| hexahistidine-encoding sequence and expressed in E. coli BL21. The | | | | |
| resulting fusion protein included an affinity tag (AAR60513) that | | | | |
| facilitated purification on Ni2+-activated NTA-agarose. A cyclic | | | | |
| procedure was used to obtain correctly folded recombinant protein. | | | | |
| (Updated on 25-MAR-2003 to correct PN field.) | | | | |
| Sequence 217 AA; | | | | |

Query Match 98.3%; Score 1029.5; DB 2; Length 217;

therapeutic, diagnostic or detection method, particularly for determining binding defects and susceptibility to a disease such as diabetes, obesity or infection; for treating acromegaly or gigantism conditions associated with lactogenic, diabetogenic, lipolytic and protein anabolic effects, conditions associated with sodium and water retention, metabolic syndromes, mood and sleep disorders; diagnosing GH dysfunction and determining pituitary storage defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH variant may also be used in the preparation of a medicament, diagnostics composition or kit, or detection kit. The method has the advantage of: expanding the know spectrum of GH1 gene mutations; evaluating the role of GH1 gene mutations in the etiology of short stature; identifying the mode of inheritance of novel lesions; evaluation the effects of GH1 mutations on the structure and function of the GH molecule and development of rapid diagnostic tests for inherited GH deficiency. This sequence is a variant of human growth hormone 1 (GH1), one of many variations of the gene discussed in the method of the invention. Note: This sequence does not appear in the specification but has been created from the GH1 wild type sequence (AAU11719) given in figure 6

Query Match 98.3%; Score 1029.5; DB 5; Length 217;
Best Local Similarity 93.1%; Pred. No. 9.6e-88;
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
QY 1 MATGRTSLLLAFGLLCLPWLOEGSAFPTPLSRFDNASLRAHRLHQLAFDYQEF 57
Db 1 MATGRTSLLLAFGLLCLPWLOEGSAFPTPLSRFDNASLRAHRLHQLAFDYQEF 60
QY 58 -----NPQTSLCFSESIPPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 105
Db 61 YIPKEQKYLFLQNPQTSLCFSESIPPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKLEEGITQMLGRLEDGSPRTGQIFKQTSKFTDTHSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKLEEGITQMLGRLEDGSPRTGQIFKQTSKFTDTHSHND 180
QY 166 ALLKNYGLLYCFRKMDKVTETFLRIVQCRSVEGSGCF 202
Db 181 ALLKNYGLLYCFRKMDKVTETFLRIVQCRSVEGSGCF 217

RESULT 4
AAU11719
ID AAU11719 standard; protein; 217 AA.

AC AAU11719;
DT 12-MAR-2002 (first entry)
DE Growth hormone 1 gene (GH1), major isoform.

DE Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;
KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;
KW water retention; metabolic syndrome; mood disorder; sleep disorder;
KW Growth hormone dysfunction; familial growth hormone deficiency;
KW short stature; pituitary storage defect; human; chromosome 17q23.

OS Homo sapiens.
XX WO200185993-A2.
XX 15-NOV-2001.
XX 14-MAY-2001; 2001WO-GB002126.
XX 12-MAY-2000; 2000GB-00011459.
XX 14-JUL-2000; 2000EP-00306004.

XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX Cooper DN, Procter AM, Gregory J, Millar DS;
PI

XX DR WPI; 2002-089798/12.
XX N-PSDB; AAS18887.

PT Detecting growth hormone variants (GH1), useful in screening patients for growth hormone irregularities, comprises comparing the nucleotide sequence of a GH1 gene from a test sample with that of a standard sequence of the human GH1.

PT Disclosure; Fig 6; 95pp; English.

XX The invention described a method of detecting variation in growth hormone 1 (GH1), and therefore GH dysfunction in an individual. The method comprises comparing the nucleotide sequence of GH1 gene obtained from the test sample with a standard human GH1 gene sequence, in order to identify variation (GH1 variant). The method is useful in screening patients for growth hormone irregularities or producing variant proteins for treating irregularities, and for the early detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in therapeutic, diagnostic or detection method, particularly for determining binding defects and susceptibility to a disease such as diabetes, obesity or infection; for treating acromegaly or gigantism conditions associated with lactogenic, diabetogenic, lipolytic and protein anabolic effects, conditions associated with sodium and water retention, metabolic syndromes, mood and sleep disorders; diagnosing GH dysfunction and determining pituitary storage defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH variant may also be used in the preparation of a medicament, diagnostics composition or kit, or detection kit. The method has the advantage of: expanding the know spectrum of GH1 gene mutations; evaluating the role of GH1 gene mutations in the etiology of short stature; identifying the mode of inheritance of novel lesions; evaluation the effects of GH1 mutations on the structure and function of the GH molecule and development of rapid diagnostic tests for inherited GH deficiency. This is the amino acid sequence of the major isoform of human growth hormone 1 (GH1), located on chromosome 17q23), used as a reference sequence for creating the mutants (AAU11721-AAU11750 and AAU11901) described in the method of the invention

XX Sequence 217 AA;

Query Match 98.3%; Score 1029.5; DB 5; Length 217;
Best Local Similarity 93.1%; Pred. No. 9.6e-88;
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
QY 1 MATGRTSLLLAFGLLCLPWLOEGSAFPTPLSRFDNASLRAHRLHQLAFDYQEF 57
Db 1 MATGRTSLLLAFGLLCLPWLOEGSAFPTPLSRFDNASLRAHRLHQLAFDYQEF 60
QY 58 -----NPQTSLCFSESIPPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 105
Db 61 YIPKEQKYLFLQNPQTSLCFSESIPPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKLEEGITQMLGRLEDGSPRTGQIFKQTSKFTDTHSHND 165
Db 121 SVFANSLVYGASDSNVYDLLKLEEGITQMLGRLEDGSPRTGQIFKQTSKFTDTHSHND 180
QY 166 ALLKNYGLLYCFRKMDKVTETFLRIVQCRSVEGSGCF 202
Db 181 ALLKNYGLLYCFRKMDKVTETFLRIVQCRSVEGSGCF 217

RESULT 5
AAU11720
ID AAU11720 standard; protein; 217 AA.

AC AAU11720;
XX 12-MAR-2002 (first entry)
XX Growth hormone 1 gene (GH1), E56G mutant.

XX Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;
KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;

| | | |
|----|---|---|
| KW | water retention; metabolic syndrome; mood disorder; sleep disorder; | |
| KW | Growth hormone dysfunction; familial growth hormone deficiency; | |
| KW | short stature; pituitary storage defect; human; mutant; mutein. | |
| XX | | |
| OS | Homo sapiens. | |
| OS | Synthetic. | |
| XX | | |
| FT | Key | Location/Qualifiers |
| FT | Misc-difference 56 | /note= "Wild type Glu substituted by Gly" |
| XX | | |
| PN | WO200185993-A2. | |
| XX | | |
| XX | 15-NOV-2001. | |
| XX | 14-MAY-2001; 2001WO-GB002126. | |
| XX | 12-MAY-2000; 2000GB-00011459. | |
| PR | 14-JUL-2000; 2000EP-00306004. | |
| XX | | |
| XX | (UYWA-) UNIV WALES COLLEGE OF MEDICINE. | |
| XX | | |
| PI | Cooper DN, Procter AM, Gregory J, Millar DS; | |
| XX | | |
| XX | WPI; 2002-089798/12. | |
| DR | N-PSDB; AAS18888. | |
| XX | | |
| XX | Detecting growth hormone variants (GHI), useful in screening patients for | |
| PT | growth hormone irregularities, comprises comparing the nucleotide | |
| PT | sequence of a GHI gene from a test sample with that of a standard | |
| PT | sequence of the human GHI. | |
| XX | | |
| XX | Claim 20; Fig 7; 95pp; English. | |
| XX | | |
| CC | The invention described a method of detecting variation in growth hormone | |
| CC | 1 (GHI), and therefore GH dysfunction in an individual. The method | |
| CC | comprises comparing the nucleotide sequence of GHI gene obtained from the | |
| CC | test sample with a standard human GHI gene sequence, in order to identify | |
| CC | variation (GHI variant). The method is useful in screening patients for | |
| CC | growth hormone irregularities or producing variant proteins for treating | |
| CC | irregularities, and for the early detection and appropriate clinical | |
| CC | management of familial GH deficiency. The GHI variants are useful in | |
| CC | therapeutic, diagnostic or detection method, particularly for determining | |
| CC | binding defects and susceptibility to a disease such as diabetes, obesity | |
| CC | or infection; for treating acromegaly or gigantism conditions associated | |
| CC | with lactogenic, diabetogenic, lipolytic and protein anabolic effects, | |
| CC | conditions associated with sodium and water retention, metabolic | |
| CC | syndromes, mood and sleep disorders; diagnosing GH dysfunction and | |
| CC | determining pituitary storage defects. The GHI variants are especially | |
| CC | useful in gene therapy or protein therapy. The GHI or GH variant may also | |
| CC | be used in the preparation of a medicament, diagnostics composition or | |
| XX | | |
| SQ | Sequence 217 AA; | |
| | Query Match 98.3%; Score 1029.5; DB 5; Length 217; | |
| | Best Local Similarity 93.1%; Pred. No. 9.6e-88; | |
| | Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1; | |
| QY | 1 MATGSTRSLLAAGLCLPWLQEGSAFPTPLSRFLDNASLRARHLQALAFDYQEF-- 57 | |
| DB | 1 MATGSTRSLLAAGLCLPWLQEGSAFPTPLSRFLDNASLRARHLQALAFDYQEGEA 60 | |
| QY | 58 -----NPTSLCFSESIPTPSNREETQOKSNLELLRISLLIQSWLEPVQFLR 105 | |

| | |
|----------|---|
| Db | 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQOKSNLELLRISLLIQSWLEPVQFLR 120 |
| QY | 106 SVFANSIVVGASDSNVYDLLKDLREGIQTILMGRLEDSGSPRTGQIFKQTSKFDNNSHDD 165 |
| Db | 121 SVFANSIVVGASDSNVYDLLKDLREGIQTILMGRLEDSGSPRTGQIFKQTSKFDNNSHDD 180 |
| QY | 166 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVEGSCGF 202 |
| Db | 181 ALLKNYGLLYCFRDKMDKVETFLRIVQCRSVEGSCGF 217 |
| | |
| RESULT 6 | |
| AAU11730 | |
| ID | AAU11730 standard; protein; 217 AA. |
| XX | |
| AC | AAU11730; |
| XX | |
| DT | 12-MAR-2002 (first entry) |
| XX | |
| DE | Growth hormone 1 gene (GHI), K67R mutant. |
| XX | |
| KW | Growth hormone 1; GHI; osteopathic; gene therapy; protein therapy; |
| KW | diabetes; obesity; infection; acromegaly; gigantism; sodium retention; |
| KW | water retention; metabolic syndrome; mood disorder; sleep disorder; |
| KW | Growth hormone dysfunction; familial growth hormone deficiency; |
| KW | short stature; pituitary storage defect; human; mutant; mutein. |
| XX | |
| OS | Homo sapiens. |
| OS | Synthetic. |
| XX | |
| FT | Key |
| FT | Misc-difference 67 |
| FT | /note= "Wild type Lys substituted by Arg" |
| XX | |
| PN | WO200185993-A2. |
| XX | |
| PD | 15-NOV-2001. |
| XX | |
| PF | 14-MAY-2001; 2001WO-GB002126. |
| XX | |
| PR | 12-MAY-2000; 2000GB-00011459. |
| PR | 14-JUL-2000; 2000EP-00306004. |
| XX | |
| XX | (UYWA-) UNIV WALES COLLEGE OF MEDICINE. |
| XX | |
| PI | Cooper DN, Procter AM, Gregory J, Millar DS; |
| XX | |
| DR | WPI; 2002-089798/12. |
| XX | |
| XX | Detecting growth hormone variants (GHI), useful in screening patients for |
| PT | growth hormone irregularities, comprises comparing the nucleotide |
| PT | sequence of a GHI gene from a test sample with that of a standard |
| PT | sequence of the human GHI. |
| XX | |
| PS | Claim 18; Page; 95pp; English. |
| XX | |
| CC | The invention described a method of detecting variation in growth hormone |
| CC | 1 (GHI), and therefore GH dysfunction in an individual. The method |
| CC | comprises comparing the nucleotide sequence of GHI gene obtained from the |
| CC | test sample with a standard human GHI gene sequence, in order to identify |
| CC | variation (GHI variant). The method is useful in screening patients for |
| CC | growth hormone irregularities or producing variant proteins for treating |
| CC | irregularities, and for the early detection and appropriate clinical |
| CC | management of familial GH deficiency. The GHI variants are useful in |
| CC | therapeutic, diagnostic or detection method, particularly for determining |
| CC | binding defects and susceptibility to a disease such as diabetes, obesity |
| CC | or infection; for treating acromegaly or gigantism conditions associated |
| CC | with lactogenic, diabetogenic, lipolytic and protein anabolic effects, |
| CC | conditions associated with sodium and water retention, metabolic |
| CC | syndromes, mood and sleep disorders; diagnosing GH dysfunction and |
| CC | determining pituitary storage defects. The GHI variants are especially |
| CC | useful in gene therapy or protein therapy. The GHI or GH variant may also |
| CC | be used in the preparation of a medicament, diagnostics composition or |
| CC | kit, or detection kit. The method has the advantage of: expanding the |
| CC | known spectrum of GHI gene mutations; evaluating the role of GHI gene |
| CC | mutations in the etiology of short stature; identifying the mode of |
| CC | inheritance of novel lesions; evaluation the effects of GHI mutations on |
| CC | the structure and function of the GH molecule and development of rapid |
| CC | diagnostic tests for inherited GH deficiency. This sequence is a variant |
| CC | of human growth hormone 1 (GHI), created from the GHI wild type sequence |
| CC | (AAU11719) given in figure 6 and one of many variations of the gene |
| CC | discussed in the method of the invention |
| XX | |

CC kit, or detection kit. The method has the advantage of: expanding the
 CC know spectrum of GH1 gene mutations; evaluating the role of GH1 gene
 CC mutations in the etiology of short stature; identifying of the mode of
 CC inheritance of novel lesions; evaluation of the effects of GH1 mutations on
 CC the structure and function of the GH molecule and development of rapid
 CC diagnostic tests for inherited GH deficiency. This sequence is a variant
 CC of human growth hormone 1 (GH1), one of many variations of the gene
 CC discussed in the method of the invention. Note: This sequence does not
 CC appear in the specification but has been created from the GH1 wild type
 CC sequence (AAU11719) given in figure 6
 XX
 SQ Sequence 217 AA;

Query Match 98.3%; Score 1029.5; DB 5; Length 217;
 Best Local Similarity 93.1%; Pred. No. 9.6e-88;
 Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
 QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFTPTPLSRFLDNASRAHRLHQLAFDTYQEF--- 57
 Db 1 MATGSRSTLLAFGLLCLPWLQEGSAFTPTPLSRFLDNASRAHRLHQLAFDTYQEFEEA 60
 QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 105
 Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 120
 QY 106 SVFANSIVYGASDSNVYDLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHND 165
 Db 121 SVFANSIVYGASDSNVYDLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHND 180
 QY 166 ALLKNYGLLYCFKMDKVFETFLRIVQCRSVGSCGF 202
 Db 181 ALLKNYGLLYCFKMDKVFETFLRIVQCRSVGSCGF 217

RESULT 7
 ABG60633
 ID ABG60633 standard; protein; 217 AA.
 XX
 AC ABG60633;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human growth hormone (hGH).
 DE
 KW Transcellular transport; transcytotic transport; paracellular transport;
 KW respiratory system disorder; lung cancer; tumour; asthma;
 KW pathogenic infection; allergy-related disorder;
 KW gastrointestinal tract disorder; gastrointestinal hormone disorder;
 KW Chron's disease; eating disorder; polyimmunoglobulin receptor; piGR.
 XX
 OS Homo sapiens.
 XX
 PN WO200228408-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US030832.
 XX
 PR 02-OCT-2000; 2000US-0237929P.
 PR 13-NOV-2000; 2000US-0248478P.
 PR 14-NOV-2000; 2000US-0248819P.
 PR 09-FEB-2001; 2001US-0267601P.
 XX
 PA (ARIZ-) ARIZEKE PHARM INC.
 XX
 PI Houston LL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;
 PI WPI; 2002-416628/44.
 DR N-PSDB; ABK81192.
 DR
 XX Complex useful for transporting active agent through epithelial barrier,
 PT has biologically active portion and target element directed to ligand
 PT that confers e.g. transcytotic properties to agent specific to ligand.

XX Disclosure; Fig 22; 379pp; English.
 XX
 CC The invention described a complex or compound (I) comprising a
 CC biologically active portion and a target element (II) directed to a
 CC ligand that confers transcellular, transcytotic or paracellular
 CC transporting properties to an agent specifically bound to the ligand,
 CC where (II) is not an antibody. Alternatively, (I) comprises two or more
 CC (II) directed to one or more ligands. (I) is useful for delivering a
 CC biologically active agent to an animal, for transporting an active agent
 CC through an epithelial or mucosal barrier, and for treating or identifying
 CC a disease in an animal e.g. diseases of the respiratory system including
 CC lung cancer and tumours, asthma, pathogenic infections, allergy-related
 CC disorders, gastrointestinal tract disorders, disorders relating to
 CC gastrointestinal hormones, Chron's disease, eating disorders and any
 CC disease or disorder involving polyimmunoglobulin receptor (piGR)
 CC displaying cells. This is the amino acid sequence of a protein associated
 CC with the transport of biologically active agents across cellular barriers
 XX
 SQ Sequence 217 AA;

Query Match 98.3%; Score 1029.5; DB 5; Length 217;
 Best Local Similarity 93.1%; Pred. No. 9.6e-88;
 Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;
 QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFTPTPLSRFLDNASRAHRLHQLAFDTYQEF--- 57
 Db 1 MATGSRSTLLAFGLLCLPWLQEGSAFTPTPLSRFLDNASRAHRLHQLAFDTYQEFEEA 60
 QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 105
 Db 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQOKSNLELLRISLLLIQSWLEPVQFLR 120
 QY 106 SVFANSIVYGASDSNVYDLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHND 165
 Db 121 SVFANSIVYGASDSNVYDLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHND 180
 QY 166 ALLKNYGLLYCFKMDKVFETFLRIVQCRSVGSCGF 202
 Db 181 ALLKNYGLLYCFKMDKVFETFLRIVQCRSVGSCGF 217

RESULT 8
 AAU11742
 ID AAU11742 standard; protein; 217 AA.
 XX
 AC AAU11742;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Growth hormone 1 gene (GH1), VI36I mutant.
 XX
 KW Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;
 KW Growth hormone dysfunction; familial growth hormone deficiency;
 KW short stature; pituitary storage defect; human; mutant; mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 136
 FT /note= "Wild type val substituted by Ile"
 XX
 PN WO200185993-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-GB002126.
 XX
 PR 12-MAY-2000; 2000GB-00011459.
 PR 14-JUL-2000; 2000EP-00306004.

Db 1 MATGSRSTLLAFGLLCLPWLQEGSAFTVPLSRFLDNASIRAHRLHQLAFDTYQEFEEA 60
 QY 58 -----NPQTSICFSESIPTPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 105
 Db 61 YIPKEQKYSFLQNFQTSICFSESIPTPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 120
 QY 106 SVFANSILVYGASDSNVYDLLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHNDD 165
 Db 121 SVFANSILVYGASDSNVYDLLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHNDD 180
 QY 166 ALLKNYGLLYCFRDMKVFTELRIVQCRSVEGSGCF 202
 Db 181 ALLKNYGLLYCFRDMKVFTELRIVQCRSVEGSGCF 217

RESULT 10

AAU11746
 ID AAU11746 standard; protein; 217 AA.
 AC AAU11746;

DT 12-MAR-2002 (first entry)

DE Growth hormone 1 gene (GHI), K194R mutant.

XX Growth hormone 1; GHI; osteopathic; gene therapy; protein therapy;
 KW diabetes; obesity; GHI; infection; acromegaly; gigantism; sodium retention;
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;
 KW Growth hormone dysfunction; familial growth hormone deficiency;
 KW short stature; pituitary storage defect; human; mutant; muten.

XX Homo sapiens.
 OS Synthetic.

PH Key Location/Qualifiers
 FT Misc-difference 194

FT /note= "Wild type Lys substituted by Arg"

PN WO200185993-A2.

PD 15-NOV-2001.

XX 14-MAY-2001; 2001WO-GB002126.

XX 12-MAY-2000; 2000GB-00011459.

PR 14-JUL-2000; 2000EP-00306004.

XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

PA Cooper DN, Procter AM, Gregory J, Millar DS;

XX WPI; 2002-089798/12.

XX Detecting growth hormone variants (GHI), useful in screening patients for
 PT growth hormone irregularities, comprises comparing the nucleotide
 PT sequence of a GHI gene from a test sample with that of a standard
 PT sequence of the human GHI.

XX Claim 18; Page; 95pp; English.

XX The invention described a method of detecting variation in growth hormone
 CC 1 (GHI), and therefore GH dysfunction in an individual. The method
 CC comprises comparing the nucleotide sequence of GHI gene obtained from the
 CC test sample with a standard human GHI gene sequence, in order to identify
 CC variation (GHI variant). The method is useful in screening patients for
 CC growth hormone irregularities or producing variant proteins for treating
 CC irregularities, and for the early detection and appropriate clinical
 CC management of familial GH deficiency. The GHI variants are useful in
 CC therapeutic, diagnostic or detection method, particularly for determining
 CC binding defects and susceptibility to a disease such as diabetes, obesity
 CC or infection; for treating acromegaly or gigantism conditions associated
 CC with lactogenic, diabetogenic, lipolytic and protein anabolic effects,
 CC conditions associated with sodium and water retention, metabolic

CC syndromes, mood and sleep disorders; diagnosing GH dysfunction and
 CC determining pituitary storage defects. The GHI variants are especially
 CC useful in gene therapy or protein therapy. The GHI or GH variant may also
 CC be used in the preparation of a medicament, diagnostics composition or
 CC kit, or detection kit. The method has the advantage of: expanding the
 CC know spectrum of GHI gene mutations; evaluating the role of GHI gene
 CC mutations in the etiology of short stature; identifying the role of GHI
 CC inheritance of novel lesions; evaluating the effects of GHI mutations on
 CC the structure and function of the GH molecule and development of rapid
 CC diagnostic tests for inherited GH deficiency. This sequence is a variant
 CC of human growth hormone 1 (GHI), one of many variations of the gene
 CC discussed in the method of the invention. Note: This sequence does not
 CC appear in the specification but has been created from the GHI wild type
 CC sequence (AAU11719) given in figure 6

XX Sequence 217 AA;

Query Match 99.0%; Score 1026.5; DB 5; Length 217;
 Best Local Similarity 92.6%; Pred. No. 1.8e-87;
 Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFTVPLSRFLDNASIRAHRLHQLAFDTYQEF--- 57

Db 1 MATGSRSTLLAFGLLCLPWLQEGSAFTVPLSRFLDNASIRAHRLHQLAFDTYQEFEEA 60

QY 58 -----NPQTSICFSESIPTPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 105

Db 61 YIPKEQKYSFLQNFQTSICFSESIPTPSNREETQOKSNLELLRLISLLLIQSWLEPVQFLR 120

QY 106 SVFANSILVYGASDSNVYDLLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHNDD 165

Db 121 SVFANSILVYGASDSNVYDLLKLEEGIQTLMGRLDGSPRTGQIFKQTSKFDNTSHNDD 180

QY 166 ALLKNYGLLYCFRDMKVFTELRIVQCRSVEGSGCF 202

Db 181 ALLKNYGLLYCFRDMKVFTELRIVQCRSVEGSGCF 217

RESULT 11

AAU11747

ID AAU11747 standard; protein; 217 AA.

AC AAU11747;

DT 12-MAR-2002 (first entry)

DE Growth hormone 1 gene (GHI), K194E mutant.

XX Growth hormone 1; GHI; osteopathic; gene therapy; protein therapy;
 KW diabetes; obesity; GHI; infection; acromegaly; gigantism; sodium retention;
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;
 KW Growth hormone dysfunction; familial growth hormone deficiency;
 KW short stature; pituitary storage defect; human; mutant; muten.

XX Homo sapiens.
 OS Synthetic.

PH Key Location/Qualifiers
 FT Misc-difference 194

FT /note= "Wild type Lys substituted by Glu"

PN WO200185993-A2.

PD 15-NOV-2001.

XX 14-MAY-2001; 2001WO-GB002126.

PR 12-MAY-2000; 2000GB-00011459.

PR 14-JUL-2000; 2000EP-00306004.

XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

XX Cooper DN, Procter AM, Gregory J, Millar DS;

PI

Db 61 YIPKEQKYSFLQNPQTSICPSESIPTSNRETTQKSNLKLRLISLLLIQSWLEPVOFLR 120
 QY 106 SVFANSILVYGASDSNVYDLLKDLLEGITQTLMGRLSDGSPRTGQIFKQYTSKFDTSNHNDD 165
 Db 121 SVFANSILVYGASDSNVYDLLKDLLEGITQTLMGRLSDGSPRTGQIFKQYTSKFDTSNHNDD 180
 QY 166 ALLKNYGLLYCFRDMKDVETFLRIVQCRSVEGSGCF 202
 Db 181 ALLKNYGLLYCFRDMKDVETFLRIVQCRSVEGSGCF 217

RESULT 13
 AAU11744
 ID AAU11744 standard; protein; 217 AA.
 AC AAU11744;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Growth hormone 1 gene (GH1), A18IV mutant.
 XX
 KW Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;
 KW Growth hormone dysfunction; familial growth hormone deficiency;
 KW short stature; pituitary storage defect; human; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 181 /note= "Wild type Ala substituted by Val"
 XX
 PN WO200185993-A2.
 XX
 XX 15-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-GB002126.
 XX
 XX 12-MAY-2000; 2000GB-00011459.
 PR 14-JUL-2000; 2000EP-00306004.
 XX
 XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX
 PI Cooper DN, Procter AM, Gregory J, Millar DS;
 XX WPI; 2002-089798/12.
 DR
 PT Detecting growth hormone variants (GH1), useful in screening patients for
 PT sequence of a GH1 gene from a test sample with that of a standard
 PT sequence of the human GH1.
 XX
 PS Claim 18; Page; 95pp; English.
 XX
 CC The invention described a method of detecting variation in growth hormone
 CC 1 (GH1), and therefore GH dysfunction in an individual. The method
 CC comprises comparing the nucleotide sequence of GH1 gene obtained from the
 CC test sample with a standard human GH1 gene sequence, in order to identify
 CC variation (GH1 variant). The method is useful in screening patients for
 CC growth hormone irregularities or producing variant proteins for treating
 CC irregularities, and for the early detection and appropriate clinical
 CC management of familial GH deficiency. The GH1 variants are useful in
 CC therapeutic, diagnostic or detection method, particularly for determining
 CC binding defects and susceptibility to a disease such as diabetes, obesity
 CC or infection; for treating acromegaly or gigantism conditions associated
 CC with lactogenic, diabetogenic, lipolytic and protein anabolic effects,
 CC conditions associated with sodium and water retention, metabolic
 CC syndromes, mood and sleep disorders; diagnosing GH dysfunction and
 CC determining pituitary storage defects. The GH1 variants are especially
 CC useful in gene therapy or protein therapy. The GH1 or GH variant may also
 CC be used in the preparation of a medicament, diagnostics composition or

CC kit, or detection kit. The method has the advantage of: expanding the
 CC know spectrum of GH1 gene mutations; evaluating the role of GH1 gene
 CC mutations in the etiology of short stature; identifying of the mode of
 CC inheritance of novel lesions; evaluation the effects of GH1 mutations on
 CC the structure and function of the GH molecule and development of rapid
 CC diagnostic tests for inherited GH deficiency. This sequence is a variant
 CC of human growth hormone 1 (GH1), one of many variations of the gene
 CC discussed in the method of the invention. Note: This sequence does not
 CC appear in the specification but has been created from the GH1 wild type
 CC sequence (AAU11719) given in figure 6
 XX
 SQ Sequence 217 AA;
 Query Match 97.9%; Score 1025.5; DB 5; Length 217;
 Best Local Similarity 92.6%; Pred. No. 2.3e-87;
 Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;
 QY 1 MATGSRISLLAFGLLCLPWLQEGSAPPTPLSRFLDNASLRAHRLHQLAFDTYQEF-- 57
 Db 1 MATGSRISLLAFGLLCLPWLQEGSAPPTPLSRFLDNASLRAHRLHQLAFDTYQEF 60
 QY 58 -----NPTSLCFSESIPTSNRETTQKSNLKLRLISLLLIQSWLEPVOFLR 105
 Db 61 YIPKEQKYSFLQNPQTSICPSESIPTSNRETTQKSNLKLRLISLLLIQSWLEPVOFLR 120
 QY 106 SVFANSILVYGASDSNVYDLLKDLLEGITQTLMGRLSDGSPRTGQIFKQYTSKFDTSNHNDD 165
 Db 121 SVFANSILVYGASDSNVYDLLKDLLEGITQTLMGRLSDGSPRTGQIFKQYTSKFDTSNHNDD 180
 QY 166 ALLKNYGLLYCFRDMKDVETFLRIVQCRSVEGSGCF 202
 Db 181 VLLKNYGLLYCFRDMKDVETFLRIVQCRSVEGSGCF 217

RESULT 14
 AAU11722
 ID AAU11722 standard; protein; 217 AA.
 XX
 AC AAU11722;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Growth hormone 1 gene (GH1), M1V mutant.
 XX
 KW Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;
 KW Growth hormone dysfunction; familial growth hormone deficiency;
 KW short stature; pituitary storage defect; human; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Wild type Met substituted by Val"
 XX
 PN WO200185993-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-GB002126.
 XX
 PR 12-MAY-2000; 2000GB-00011459.
 PR 14-JUL-2000; 2000EP-00306004.
 XX
 XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX
 PI Cooper DN, Procter AM, Gregory J, Millar DS;
 XX WPI; 2002-089798/12.
 DR
 XX Detecting growth hormone variants (GH1), useful in screening patients for

PT growth hormone irregularities, comprises comparing the nucleotide
PT sequence of a GH1 gene from a test sample with that of a standard
XX sequence of the human GH1.
PS Claim 18; Page; 95pp; English.
XX
XX The invention described a method of detecting variation in growth hormone
CC 1 (GH1), and therefore GH dysfunction in an individual. The method
CC comprises comparing the nucleotide sequence of GH1 gene obtained from the
CC test sample with a standard human GH1 gene sequence, in order to identify
CC variation (GH1 variant). The method is useful in screening patients for
CC growth hormone irregularities or producing variant proteins for treating
CC irregularities, and for the early detection and appropriate clinical
CC management of familial GH deficiency. The GH1 variants are useful in
CC therapeutic, diagnostic or detection method, particularly for determining
CC binding defects and susceptibility to a disease such as diabetes, obesity
CC or infection; for treating acromegaly or gigantism conditions associated
CC with lactogenic, diabetogenic, lipolytic and protein anabolic effects,
CC conditions associated with sodium and water retention, metabolic
CC syndromes, mood and sleep disorders; diagnosing GH dysfunction and
CC determining pituitary storage defects. The GH1 variants are especially
CC useful in gene therapy or protein therapy. The GH1 or GH variant may also
CC be used in the preparation of a medicament, diagnostics composition or
CC kit, or detection kit. The method has the advantage of: expanding the
CC know spectrum of GH1 gene mutations; evaluating the role of GH1 gene
CC mutations in the etiology of short stature; identifying of the mode of
CC inheritance of novel lesions; evaluation the effects of GH1 mutations on
CC the structure and function of the GH molecule and development of rapid
CC diagnostic tests for inherited GH deficiency. This sequence is a variant
CC of human growth hormone 1 (GH1), one of many variations of the gene
CC discussed in the method of the invention. Note: This sequence does not
CC appear in the specification but has been created from the GH1 wild type
CC sequence (AAU11719) given in figure 6
XX
XX Sequence 217 AA;
Query Match 97.9%; Score 1025.5; DB 5; Length 217;
Best Local Similarity 92.6%; Pred. No. 2.3e-87;
Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;
QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTPLSRFLDNASRAHRLHQLAFDTYQEF--- 57
DB 1 VATGSRSTLLAFGLLCLPWLQEGSAFPTPLSRFLDNASRAHRLHQLAFDTYQEF 60
QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELRISLLIQSWLEPVQFLR 105
DB 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQOKSNLELRISLLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKDLERGIOTLMGRLEDGSPRTQIFKQYKSFDTNSHND 165
DB 121 SVFANSLVYGASDSNVYDLLKDLERGIOTLMGRLEDGSPRTQIFKQYKSFDTNSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSGCF 202
DB 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSGCF 217
RESULT 15
AAU11728
ID AAU11728 standard; protein; 217 AA.
XX
XX AAU11728;
XX
XX 12-MAR-2002 (first entry)
DE Growth hormone 1 gene (GH1), Q48R mutant.
XX
XX Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;
KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;
KW water retention; metabolic syndrome; mood disorder; sleep disorder;
KW Growth hormone dysfunction; familial growth hormone deficiency;
KW short stature; pituitary storage defect; human; mutant; mutain.
XX

OS Homo sapiens.
OS Synthetic.
PH Key Location/Qualifiers
FT Misc-difference 48 /note= "Wild type Gln substituted by Arg"
FT
XX WC200185993-A2.
XX
XX 15-NOV-2001.
XX 14-MAY-2001; 2001WO-GH002126.
XX 12-MAY-2000; 2000GB-00011459.
XX 14-JUL-2000; 2000EP-00306004.
XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX Cooper DN, Procter AM, Gregory J, Millar DS;
XX WPI; 2002-089798/12.
XX Detecting growth hormone variants (GH1), useful in screening patients for
XX growth hormone irregularities, comprises comparing the nucleotide
XX sequence of a GH1 gene from a test sample with that of a standard
XX sequence of the human GH1.
XX Claim 18; Page; 95pp; English.
XX The invention described a method of detecting variation in growth hormone
XX 1 (GH1), and therefore GH dysfunction in an individual. The method
XX comprises comparing the nucleotide sequence of GH1 gene obtained from the
XX test sample with a standard human GH1 gene sequence, in order to identify
XX variation (GH1 variant). The method is useful in screening patients for
XX growth hormone irregularities or producing variant proteins for treating
XX irregularities, and for the early detection and appropriate clinical
XX management of familial GH deficiency. The GH1 variants are useful in
XX therapeutic, diagnostic or detection method, particularly for determining
XX binding defects and susceptibility to a disease such as diabetes, obesity
XX or infection; for treating acromegaly or gigantism conditions associated
XX with lactogenic, diabetogenic, lipolytic and protein anabolic effects,
XX conditions associated with sodium and water retention, metabolic
XX syndromes, mood and sleep disorders; diagnosing GH dysfunction and
XX determining pituitary storage defects. The GH1 variants are especially
XX useful in gene therapy or protein therapy. The GH1 or GH variant may also
XX be used in the preparation of a medicament, diagnostics composition or
XX kit, or detection kit. The method has the advantage of: expanding the
XX know spectrum of GH1 gene mutations; evaluating the role of GH1 gene
XX mutations in the etiology of short stature; identifying of the mode of
XX inheritance of novel lesions; evaluation the effects of GH1 mutations on
XX the structure and function of the GH molecule and development of rapid
XX diagnostic tests for inherited GH deficiency. This sequence is a variant
XX of human growth hormone 1 (GH1), one of many variations of the gene
XX discussed in the method of the invention. Note: This sequence does not
XX appear in the specification but has been created from the GH1 wild type
XX sequence (AAU11719) given in figure 6
XX
XX Sequence 217 AA;
Query Match 97.9%; Score 1025.5; DB 5; Length 217;
Best Local Similarity 92.6%; Pred. No. 2.3e-87;
Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;
QY 1 MATGSRSTLLAFGLLCLPWLQEGSAFPTPLSRFLDNASRAHRLHQLAFDTYQEF--- 57
DB 1 VATGSRSTLLAFGLLCLPWLQEGSAFPTPLSRFLDNASRAHRLHQLAFDTYQEF 60
QY 58 -----NPQTSLCFSESIPTPSNREETQOKSNLELRISLLIQSWLEPVQFLR 105
DB 61 YIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQOKSNLELRISLLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLLKDLERGIOTLMGRLEDGSPRTQIFKQYKSFDTNSHND 165
DB 121 SVFANSLVYGASDSNVYDLLKDLERGIOTLMGRLEDGSPRTQIFKQYKSFDTNSHND 180
QY 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSGCF 202
DB 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVEGSGCF 217
RESULT 15
AAU11728
ID AAU11728 standard; protein; 217 AA.
XX
XX AAU11728;
XX
XX 12-MAR-2002 (first entry)
DE Growth hormone 1 gene (GH1), Q48R mutant.
XX
XX Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;
KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;
KW water retention; metabolic syndrome; mood disorder; sleep disorder;
KW Growth hormone dysfunction; familial growth hormone deficiency;
KW short stature; pituitary storage defect; human; mutant; mutain.
XX

Db 121 SVFANSUVYGASDSNVYDLLKDLLEEGIQTLMGRLDGSPRTGQIFKQYISKFDTNSHDD 180
Qy 166 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVGSCGF 202
Db 181 ALLKNYGLLYCFRKMDKVETFLRIVQCRSVGSCGF 217

Search completed: July 12, 2004, 13:03:54
Job time : 63 secs

